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Val Pro His Leu Ile Leu Ile Ala Ser Arg Asp Ile Ala Ala Gly Glu	
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Glu Leu Leu Tyr Asp Tyr Gly Asp Arg Ser Lys Ala Ser Ile Glu Ala	
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His Pro Trp Leu Lys His *	
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Ile Glu Ser Gly Gln Leu Arg Leu Val Asn Gly Gly Arg Cys Ala	
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1002				1007				1012			1017					
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Cys	Gly	His	Lys	Glu	Asp	Ala	Ala	Val	Asn	Cys	Thr	Asp	Ile	Ser	Val	
1018				1023				1028			1033					
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Gln	Lys	Thr	Pro	Gln	Lys	Ala	Thr	Thr	Gly	Arg	Ser	Ser	Arg	Gln	Ser	
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Val	Ala	Leu	Phe	Leu	Thr	Lys	Lys	Arg	Arg	Gln	Arg	Gln	Arg	Leu		
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Lys His His Glu Trp Gly Lys His Tyr Cys Asn His Asn Glu Asp Ala			
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362	367	372	377
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Leu Gly Lys Val Cys Asp Arg Gly Trp Gly Leu Lys Glu Ala Asp Val			
394	399	404	409
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Val Cys Arg Gln Leu Gly Cys Gly Ser Ala Leu Lys Thr Ser Tyr Gln			
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Val Tyr Ser Lys Ile Gln Ala Thr Asn Thr Trp Leu Phe Leu Ser Ser			
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gga cag atc tgg gct gaa gaa ttc cag tgt gag gga cat gag tcc cat			1745
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agg cac aag gag gat gcg gga gtt atc tgc tca gaa ttc atg tct ctg Arg His Lys Glu Asp Ala Gly Val Ile Cys Ser Glu Phe Met Ser Leu 842 847 852 857	2657
aga ctg acc agt gaa gcc agc aga gag gcc tgt gca ggg cgt ctg gaa Arg Leu Thr Ser Glu Ala Ser Arg Glu Ala Cys Ala Gly Arg Leu Glu 858 863 868 873	2705
gtt ttt tac aat gga gct tgg ggc act gtt ggc aag agt agc atg tct Val Phe Tyr Asn Gly Ala Trp Gly Thr Val Gly Lys Ser Ser Met Ser 874 879 884 889	2753
gaa acc act gtg ggt gtg tgc agg cag ctg ggc tgt gca gac aaa Glu Thr Thr Val Gly Val Cys Arg Gln Leu Gly Cys Ala Asp Lys 890 895 900 905	2801
ggg aaa atc aac cct gca tct tta gac aag gcc atg tcc att ccc atg Gly Lys Ile Asn Pro Ala Ser Leu Asp Lys Ala Met Ser Ile Pro Met 906 911 916 921	2849
tgg gtg gac aat gtt cag tgt cca aaa gga cct gac acg ctg tgg cag Trp Val Asp Asn Val Gln Cys Pro Lys Gly Pro Asp Thr Leu Trp Gln 922 927 932 937	2897
tgc cca tca tct cca tgg gag aag aga ctg gcc agc ccc tcg gag gag Cys Pro Ser Ser Pro Trp Glu Lys Arg Leu Ala Ser Pro Ser Glu Glu 938 943 948 953	2945
acc tgg atc aca tgt gac aac aag ata aga ctt cag gaa gga ccc act Thr Trp Ile Thr Cys Asp Asn Lys Ile Arg Leu Gln Glu Gly Pro Thr 954 959 964 969	2993
tcc tgt tct gga cgt gtg gag atc tgg cat gga ggt tcc tgg ggg aca Ser Cys Ser Gly Arg Val Glu Ile Trp His Gly Gly Ser Trp Gly Thr 970 975 980 985	3041
gtg tgt gat gac tct tgg gac ttg gac gat gct cag gtg gtg tgt caa Val Cys Asp Asp Ser Trp Asp Leu Asp Asp Ala Gln Val Val Cys Gln 986 991 996 1001	3089
caa ctt ggc tgt ggt cca gct ttg aaa gca ttc aaa gaa gca gag ttt Gln Leu Gly Cys Gly Pro Ala Leu Lys Ala Phe Lys Glu Ala Glu Phe 1002 1007 1012 1017	3137

ggt cag ggg act gga ccg ata tgg ctc aat gaa gtg aag tgc aaa ggg Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu Val Lys Cys Lys Gly 1018 1023 1028 1033	3185
aat gag tct tcc ttg tgg gat tgt cct gcc aga cgc tgg ggc cat agt Asn Glu Ser Ser Leu Trp Asp Cys Pro Ala Arg Arg Trp Gly His Ser 1034 1039 1044 1049	3233
gag tgt ggg cac aag gaa gac gct gca gtg aat tgc aca gat att tca Glu Cys Gly His Lys Glu Asp Ala Ala Val Asn Cys Thr Asp Ile Ser 1050 1055 1060 1065	3281
gtg cag aaa acc cca caa aaa gcc aca aca ggt cgc tca tcc cgt cag Val Gln Lys Thr Pro Gln Lys Ala Thr Thr Gly Arg Ser Ser Arg Gln 1066 1071 1076 1081	3329
tca tcc ttt att gca gtc ggg atc ctt ggg gtt gtt ctg ttg gcc att Ser Ser Phe Ile Ala Val Gly Ile Leu Gly Val Val Leu Leu Ala Ile 1082 1087 1092 1097	3377
ttc gtc gca tta ttc ttc ttg act aaa aag cga aga cag aga cag cgg Phe Val Ala Leu Phe Phe Leu Thr Lys Lys Arg Arg Gln Arg Gln Arg 1098 1103 1108 1113	3425
ctt gca gtt tcc tca aga gga gag aac tta gtc cac caa att caa tac Leu Ala Val Ser Ser Arg Gly Glu Asn Leu Val His Gln Ile Gln Tyr 1114 1119 1124 1129	3473
cg ^g gag atg aat tct tgc ctg aat gca gat gat ctg gac cta atg aat Arg Glu Met Asn Ser Cys Leu Asn Ala Asp Asp Leu Asp Leu Met Asn 1130 1135 1140 1145	3521
tcc tca gga ggc cat tct gag cca cac tga a aaggaaaaatg ggaatttata Ser Ser Gly Gly His Ser Glu Pro His *	3572
1146 1151	
acccagttag ttcagcccttt aagatacctt gatgaagacc tggactattg aatggagcag aaattcacct ctctcactga ctattacagt tgcattttta tggagttctt cttctcctag	3632
gattcctaag actgctgctg aatttataaa aattaagttt gtgaatgtga ctacttagtg	3692
gtgtatatga gactttcaag ggaattaaat aaataaataa gaatgttaaa aaaaaaaaaa	3752
	3811

<210> 539
 <211> 1865
 <212> DNA
 <213> Homo sapiens

<220> |
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 <222> (218)..(1120)

<400> 539

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actaccgttc ccggcatgcc atgaaattgg cctccggcgt gaggcggggt ccggccctcc	180
acccgctccc gccgcgcgcg aatcgccgtc gcgagcc atg gag gag gca tcg Met Glu Glu Ala Ser	235
1	
tcc ccg ggg ctg ggc tgc agc aag ccg cac ctg gag aag ctg acc ctg Ser Pro Gly Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu	283
7 12 17 22	
ggc atc acg cgc atc cta gaa tct tcc cca ggt gtg act gag gtg acc Gly Ile Thr Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr	331
23 28 33 38	
atc ata gaa aag cct cct gct gaa cgt cat atg att tct tcc tgg gaa Ile Ile Glu Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu	379
39 44 49 54	
caa aag aat aac tgt gtg atg cct gaa gat gtg aag aac ttt tac ctg Gln Lys Asn Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu	427
55 60 65 70	
atg acc aat ggc ttc cac atg aca tgg agt gtg aag ctg gat gag cac Met Thr Asn Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Glu His	475
71 76 81 86	
atc att cca ctg gga agc atg gca att aac agc atc tca aaa ctg act Ile Ile Pro Leu Gly Ser Met Ala Ile Asn Ser Ile Ser Lys Leu Thr	523
87 92 97 102	
cag ctc acc cag tct tcc atg tat tca ctt cct aat gca ccc act ctg Gln Leu Thr Gln Ser Ser Met Tyr Ser Leu Pro Asn Ala Pro Thr Leu	571
103 108 113 118	
gca gac ctg gag gac gat aca cat gaa gcc agt gat gat cag cca gag Ala Asp Leu Glu Asp Asp Thr His Glu Ala Ser Asp Asp Gln Pro Glu	619
119 124 129 134	
aag cct cac ttt gac tct cgc agt gtg ata ttt gag ctg gat tca tgc Lys Pro His Phe Asp Ser Arg Ser Val Ile Phe Glu Leu Asp Ser Cys	667
135 140 145 150	
aat ggc agt ggg aaa gtt tgc ctt gtc tac aaa agt ggg aaa cca gca Asn Gly Ser Gly Lys Val Cys Leu Val Tyr Lys Ser Gly Lys Pro Ala	715
151 156 161 166	
tta gca gaa gac act gag atc tgg ttc ctg gac aga gcg tta tac tgg Leu Ala Glu Asp Thr Glu Ile Trp Phe Leu Asp Arg Ala Leu Tyr Trp	763
167 172 177 182	
cat ttt ctc aca gac acc ttt act gcc tat tac cgc ctg ctc atc acc His Phe Leu Thr Asp Thr Phe Thr Ala Tyr Tyr Arg Leu Leu Ile Thr	811
183 188 193 198	

cac ctg ggc ctg ccc cag tgg caa tat gcc ttc acc agc tat ggc att	859
His Leu Gly Leu Pro Gln Trp Gln Tyr Ala Phe Thr Ser Tyr Gly Ile	
199 204 209 214	
agc cca cag gcc aag caa tgg ttc agc atg tat aaa cct atc acc tac	907
Ser Pro Gln Ala Lys Gln Trp Phe Ser Met Tyr Lys Pro Ile Thr Tyr	
215 220 225 230	
aac aca aac ctg ctc aca gaa gag acc gac tcc ttt gtg aat aag cta	955
Asn Thr Asn Leu Leu Thr Glu Glu Thr Asp Ser Phe Val Asn Lys Leu	
231 236 241 246	
gat ccc agc aaa gtg ttt aag agc aag aac aag atc gta atc cca aaa	1003
Asp Pro Ser Lys Val Phe Lys Ser Lys Asn Lys Ile Val Ile Pro Lys	
247 252 257 262	
aag aaa ggg cct gtg cag cct gca ggt ggc cag aaa ggg ccc tca gga	1051
Lys Lys Gly Pro Val Gln Pro Ala Gly Gly Gln Lys Gly Pro Ser Gly	
263 268 273 278	
ccc tcc ggt ccc tcc act tcc tcc act tct aaa tcc tcc tct ggc tct	1099
Pro Ser Gly Pro Ser Thr Ser Ser Thr Ser Lys Ser Ser Ser Gly Ser	
279 284 289 294	
gga aac ccc acc cgg aag tga gc acccctccct ccaactccct accagctcca	1152
Gly Asn Pro Thr Arg Lys *	
295 300	
gagtgggtgg ttcctatgcac agatggccct aggggtgacc tccagtttg cgtgtggacc	1212
gtaggcctct ttcttagttga atgaccaaaa ttgttaaggct tttagtccca ccgacattag	1272
ccaggctcgt agtgaggccct ccagagcagg ttgtgctgtc ccctgcctct ggaagcaatg	1332
ggaaatttgg aatcttgtgt aagtgcctaa ataagtctga gtgcttcct cttttcaac	1392
actcaaccct caatccctta gcactgattt attagagagg tccccaaag aaaccactgg	1452
tttgaccca tgaagcatta gaactgcatt gttcattcag gagccactag tcacatatga	1512
ctattnaat tttaagtaaa ttgtatgaaa aattcatttc ttcaatttca tttagccacat	1572
tttgagttt catgtggctg gtagattctg tattagcaca aagatatgga acatttccat	1632
caccacagaa agttctgttg gacagcactg cattagaata ttttctact gctcttcctc	1692
aattaatttt tggtgttaat gttgatgtct tcattggatg ggtcataatg ttccatgaaa	1752
cctctcaagt acacaattgt atgttctttg tatcccttac cacaaatatc tcgctctgct	1812
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<211> 1736
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (218)..(991)

 <400> 540
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 actaccgttc cggcatgcc atgaaattgg cctcggcgct gaggcggggt cggccctcc 180
 acccgcgtccc gccgcgcgcg aatcgccgtc gcgagcc atg gag gag gag gca tcg 235
 Met Glu Glu Glu Ala Ser
 1

 tcc ccg ggg ctg ggc tgc agc aag ccg cac ctg gag aag ctg acc ctg 283
 Ser Pro Gly Leu Gly Cys Ser Lys Pro His Leu Glu Lys Leu Thr Leu
 7 12 17 22

 ggc atc acg cgc atc cta gaa tct tcc cca ggt gtg act gag gtg acc 331
 Gly Ile Thr Arg Ile Leu Glu Ser Ser Pro Gly Val Thr Glu Val Thr
 23 28 33 38

 atc ata gaa aag cct cct gct gaa cgt cat atg att tct tcc tgg gaa 379
 Ile Ile Glu Lys Pro Pro Ala Glu Arg His Met Ile Ser Ser Trp Glu
 39 44 49 54

 caa aag aat aac tgt gtg atg cct gaa gat gtg aag aac ttt tac ctg 427
 Gln Lys Asn Asn Cys Val Met Pro Glu Asp Val Lys Asn Phe Tyr Leu
 55 60 65 70

 atg acc aat ggc ttc cac atg aca tgg agt gtg aag ctg gat gcc agt 475
 Met Thr Asn Gly Phe His Met Thr Trp Ser Val Lys Leu Asp Ala Ser
 71 76 81 86

 gat gat cag cca gag aag cct cac ttt gac tct cgc agt gtg ata ttt 523
 Asp Asp Gln Pro Glu Lys Pro His Phe Asp Ser Arg Ser Val Ile Phe
 87 92 97 102

 gag ctg gat tca tgc aat ggc agt ggg aaa gtt tgc ctt gtc tac aaa 571
 Glu Leu Asp Ser Cys Asn Gly Ser Gly Lys Val Cys Leu Val Tyr Lys
 103 108 113 118

 agt ggg aaa cca gca tta gca gaa gac act gag atc tgg ttc ctg gac 619
 Ser Gly Lys Pro Ala Leu Ala Glu Asp Thr Glu Ile Trp Phe Leu Asp
 119 124 129 134

 aga gcg tta tac tgg cat ttt ctc aca gac acc ttt act gcc tat tac 667
 Arg Ala Leu Tyr Trp His Phe Leu Thr Asp Thr Phe Thr Ala Tyr Tyr
 135 140 145 / 150

 cgc ctg ctc atc acc cac ctg ggc ctg ccc cag tgg caa tat gcc ttc 715
 Arg Leu Leu Ile Thr His Leu Gly Leu Pro Gln Trp Gln Tyr Ala Phe

151	156	161	166	
acc agc tat ggc att agc cca cag gcc aag caa tgg ttc agc atg tat				763
Thr Ser Tyr Gly Ile Ser Pro Gln Ala Lys Gln Trp Phe Ser Met Tyr				
167	172	177	182	
aaa cct atc acc tac aac aca aac ctg ctc aca gaa gag acc gac tcc				811
Lys Pro Ile Thr Tyr Asn Thr Asn Leu Leu Thr Glu Glu Thr Asp Ser				
183	188	193	198	
ttt gtg aat aag cta gat ccc agc aaa gtg ttt aag agc aag aac aag				859
Phe Val Asn Lys Leu Asp Pro Ser Lys Val Phe Lys Ser Lys Asn Lys				
199	204	209	214	
atc gta atc cca aaa aag aaa ggg cct gtg cag cct gca ggt ggc cag				907
Ile Val Ile Pro Lys Lys Gly Pro Val Gln Pro Ala Gly Gly Gln				
215	220	225	230	
aaa ggg ccc tca gga ccc tcc ggt ccc tcc act tcc tcc act tct aaa				955
Lys Gly Pro Ser Gly Pro Ser Gly Pro Ser Thr Ser Ser Thr Ser Lys				
231	236	241	246	
tcc tcc tct ggc tct gga aac ccc acc cgg aag tga gcac ccctccctcc				1005
Ser Ser Ser Gly Ser Gly Asn Pro Thr Arg Lys *				
247	252	257		
aactccctac cagctccaga gtgggtggttt ccatgcacag atggccctag gggtgacctc				1065
cagttttgcg tgtggaccgt aggcctctt ctagttgaat gaccaaaatt gtaaggcttt				1125
tagtcccacc gacatttagcc aggctcgtag tgaggcctcc agagcaggtt gtgtgtccc				1185
ctgcctctgg aagcaatggg gaatttggaa tcttgtgtaa gtgcccaaatt aagtctgagt				1245
gctttcctct tcttcaacac tcaaccctca atcccttagc actgattgtat tagagaggtc				1305
ccccaaagaa accactggtt ttgacccatg aagcattaga actgcattgt tcattcagga				1365
gccactagtc acatatgact atttaaattt aaagtaaattt gtatgaaaaa ttcatatttt				1425
caattgcatt agccacattt ttagtattca tgtggctggt agattctgta ttagcacaaa				1485
gatatggaac atttccatca ccacagaaag ttctgttgaa cagcactgca tttagaatatt				1545
ttcatactgc tcttcctcaa ttaatttttgg ttagttaatgt ttagtgccttc attggatggg				1605
tcataatgtt ccatgaaacc tctcaagtac acaattgtat gttctttgtat tcccttacca				1665
caaatatctc gctctgctca tttctttgc agcttcctat aaagtttgc ttcctcatca				1725
aaaaaaaaaa a				1736

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<210> 541
<211> 563

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (185)..(460)

<400> 541

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cgtgggttgg	gtcgtacttg	ggacctcggc	gaagaggacc	cgtttatttt	tttttcttcc	180	
caaa atg gca	gcc tcc agt	cgc gca	caa gtg	tta tct	ctg tac	cgg gcg	229
Met Ala Ala	Ser Ser Arg	Ala Gln	Val Leu	Ser Leu	Tyr Arg	Ala	
1	5	10					
atg ctg aga	gag agc aag	cgt ttc	agc gcc	tac aat	tac aga	aca tat	277
Met Leu Arg	Glu Ser Lys	Arg Phe	Ser Ala	Tyr Asn	Tyr Arg	Thr Tyr	
16	21	26	31				
gct gtc agg	agg ata aga	gat gcc	ttc aga	gaa aat	aaa aat	gta aag	325
Ala Val Arg	Arg Ile Arg	Asp Ala	Phe Arg	Glu Asn	Lys Asn	Val Lys	
32	37	42	47				
gat cct gta	gaa att caa acc	cta gtg	aat aaa	gcc aag	aga gac	ctt	373
Asp Pro Val	Glu Ile Gln	Thr Leu Val	Asn Lys	Ala Lys	Arg Asp	Leu	
48	53	58	63				
gga gta att	cgt cga cag	gtc cac	att ggc	caa ctg	tat tca	act gac	421
Gly Val Ile	Arg Arg Gln	Val His Ile	Gly Gln	Leu Tyr	Ser Thr	Asp	
64	69	74	79				
aag ctg atc	att gag aat	cga gac	atg ccc	agg acc	tag caagccgggg		470
Lys Leu Ile	Ile Glu Asn	Arg Asp Met	Pro Arg	Thr	*		
80	85	90					
accagccacc	agtggcgccc	agggaccacc	ttcagcatcc	actctctgtt	tgagctgggg		530
gctcccaaaa	ccagcttaca	atagcctttt	gcg				563

<210> 542
<211> 2100
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (33)..(1835)

<400> 542

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				Met Pro	Glu Ile Arg Val	Thr

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ccc ttg ggg gcc ggc cag gac gtg ggc cga agc tgc atc ctg gtc tcc Pro Leu Gly Ala Gly Gln Asp Val Gly Arg Ser Cys Ile Leu Val Ser	8	13	18
			23
att gcg ggc aag aat gtc atg ctg gac tgt gga atg cac atg ggc ttc Ile Ala Gly Lys Asn Val Met Leu Asp Cys Gly Met His Met Gly Phe	24	29	34
			39
aat gac gac cga cgc ttc cct gac ttc tcc tac atc acc cag aac ggc Asn Asp Asp Arg Arg Phe Pro Asp Phe Ser Tyr Ile Thr Gln Asn Gly	40	45	50
			55
cgc cta aca gac ttc ctg gac tgt gtg atc att agc cac ttc cac ctg Arg Leu Thr Asp Phe Leu Asp Cys Val Ile Ile Ser His Phe His Leu	56	61	66
			71
gac cac tgc ggg gca ctc ccc tac ttc agc gag atg gtg ggc tac gac Asp His Cys Gly Ala Leu Pro Tyr Phe Ser Glu Met Val Gly Tyr Asp	72	77	82
			87
ggc ccc atc tac atg act cac ccc acc cag gcc atc tgc ccc atc ttg Gly Pro Ile Tyr Met Thr His Pro Thr Gln Ala Ile Cys Pro Ile Leu	88	93	98
			103
ctg gag gac tac cgc aag atc gcc gta gac aag aag ggc gag gcc aac Leu Glu Asp Tyr Arg Lys Ile Ala Val Asp Lys Lys Gly Glu Ala Asn	104	109	114
			119
tcc ttc acc tcc cag atg atc aaa gac tgc atg aag aag gtg gtg gct Phe Phe Thr Ser Gln Met Ile Lys Asp Cys Met Lys Lys Val Val Ala	120	125	130
			135
gtc cac ctc cac cag acg gtc cag gta gat gat gag ctg gag atc aag Val His Leu His Gln Thr Val Gln Val Asp Asp Glu Leu Glu Ile Lys	136	141	146
			151
gcc tac tat gca ggc cac gtg ctg ggg gca gcc atg ttc cag att aaa Ala Tyr Tyr Ala Gly His Val Leu Gly Ala Ala Met Phe Gln Ile Lys	152	157	162
			167
gtg ggc tca gag tct gtg gtc tac acg ggt gat tat aac atg acc cca Val Gly Ser Glu Ser Val Val Tyr Thr Gly Asp Tyr Asn Met Thr Pro	168	173	178
			183
gac cga cac tta gga gct gcc tgg att gac aag tgc cgc ccc aac ctg Asp Arg His Leu Gly Ala Ala Trp Ile Asp Lys Cys Arg Pro Asn Leu	184	189	194
			199
ctc atc aca gag tcc acg tac gcc acg acc atc cgt gac tcc aag cgc Leu Ile Thr Glu Ser Thr Tyr Ala Thr Thr Ile Arg Asp Ser Lys Arg	200	205	210
			215
tgc cgg gag cga gac ttc ctg aag aaa gtc cac gag acc gtg gag cgt Cys Arg Glu Arg Asp Phe Leu Lys Lys Val His Glu Thr Val Glu Arg	216	221	226
			231

ggt ggg aag gtg ctg ata cct gtg ttc gcg ctg ggc cgc gcc cag gag	773
Gly Gly Lys Val Leu Ile Pro Val Phe Ala Leu Gly Arg Ala Gln Glu	
232 237 242 247	
ctc tgc atc ctc ctg gag acc ttc tgg gag cgc atg aac ctg aag gtg	821
Leu Cys Ile Leu Leu Glu Thr Phe Trp Glu Arg Met Asn Leu Lys Val	
248 253 258 263	
ccc atc tac ttc tcc acg ggg ctg acc gag aag gcc aac cac tac tac	869
Pro Ile Tyr Phe Ser Thr Gly Leu Thr Glu Lys Ala Asn His Tyr Tyr	
264 269 274 279	
aag ctg ttc atc ccc tgg acc aac cag aag atc cgc aag act ttc gtg	917
Lys Leu Phe Ile Pro Trp Thr Asn Gln Lys Ile Arg Lys Thr Phe Val	
280 285 290 295	
cag agg aac atg ttt gag ttc aag cac atc aag gcc ttc gac cgg gct	965
Gln Arg Asn Met Phe Glu Phe Lys His Ile Lys Ala Phe Asp Arg Ala	
296 301 306 311	
ttt gct gac aac cca gga ccg atg gtt gtg ttt gcc acg cca gga atg	1013
Phe Ala Asp Asn Pro Gly Pro Met Val Val Phe Ala Thr Pro Gly Met	
312 317 322 327	
ctg cac gct ggg cag tcc ctg cag atc ttc ccg aaa tgg gcc gga aac	1061
Leu His Ala Gly Gln Ser Leu Gln Ile Phe Arg Lys Trp Ala Gly Asn	
328 333 338 343	
gaa aag aac atg gtc atc atg ccc ggc tac tgc gtg cag ggc acc gtc	1109
Glu Lys Asn Met Val Ile Met Pro Gly Tyr Cys Val Gln Gly Thr Val	
344 349 354 359	
ggc cac aag atc ctc agc ggg cag ccg aag ctc gag atg gag ggg ccg	1157
Gly His Lys Ile Leu Ser Gly Gln Arg Lys Leu Glu Met Glu Gly Arg	
360 365 370 375	
cag gtg ctg gag gtc aag atg cag gtg gag tac atg tca ttc agc gca	1205
Gln Val Leu Glu Val Lys Met Gln Val Glu Tyr Met Ser Phe Ser Ala	
376 381 386 391	
cac gcg gac gcc aag ggc atc atg cag ctg gtg ggc cag gca gag ccg	1253
His Ala Asp Ala Lys Gly Ile Met Gln Leu Val Gly Gln Ala Glu Pro	
392 397 402 407	
gag agc gtg ctg ctg gtg cat ggc gag gcc aag aag atg gag ttc ctg	1301
Glu Ser Val Leu Leu Val His Gly Glu Ala Lys Lys Met Glu Phe Leu	
408 413 418 423	
aag cag aag atc gag cag gag ctc cgg gtc aac tgc tac atg ccg gcc	1349
Lys Gln Lys Ile Glu Gln Glu Leu Arg Val Asn Cys Tyr Met Pro Ala	
424 429 434 439	
aat ggc gag acg gtg acg ctg ccc aca agc ccc agc atc ccc gta ggc	1397
Asn Gly Glu Thr Val Thr Leu Pro Thr Ser Pro Ser Ile Pro Val Gly	
440 445 450 455	

atc tcg ctg ggg ctg ctg aag cg ^g gag atg gc ^g cag ggg ctg ctc cct Ile Ser Leu Gly Leu Leu Lys Arg Glu Met Ala Gln Gly Leu Leu Pro	1445
456 461 466 471	
gag gcc aag aag cct cg ^g ctc ctg cac gg ^c acc ctg atc atg aag gac Glu Ala Lys Lys Pro Arg Leu Leu His Gly Thr Leu Ile Met Lys Asp	1493
472 477 482 487	
agc aac ttc cg ^g ctg gt ^g tcc tca gag c ^a a gcc ctc aaa gag ctg gg ^t Ser Asn Phe Arg Leu Val Ser Ser Glu Gln Ala Leu Lys Glu Leu Gly	1541
488 493 498 503	
ctg gct gag cac cag ctg cg ^c ttc acc tgc cg ^c gt ^g cac ctg cat gac Leu Ala Glu His Gln Leu Arg Phe Thr Cys Arg Val His Leu His Asp	1589
504 509 514 519	
aca cg ^c aag gag cag gag acg gca ttg cg ^c gtc tac agc cac ctc aag Thr Arg Lys Glu Gln Glu Thr Ala Leu Arg Val Tyr Ser His Leu Lys	1637
520 525 530 535	
agc gtc ctg aag gac cac tgt gt ^g cag cac ctc cca gac gg ^c tct gt ^g Ser Val Leu Lys Asp His Cys Val Gln His Leu Pro Asp Gly Ser Val	1685
536 541 546 551	
act gt ^g gag tcc gtc ctc ctc cag gg ^c gg ^c cct tct gag gac cca Thr Val Glu Ser Val Leu Leu Gln Ala Ala Pro Ser Glu Asp Pro	1733
552 557 562 567	
ggc acc aag gt ^g ctg ctg gtc tcc tgg acc tac cag gac gag gag ctg Gly Thr Lys Val Leu Leu Val Ser Trp Thr Tyr Gln Asp Glu Glu Leu	1781
568 573 578 583	
ggg agc ttc ctc aca tct ctg ctg aag aag gg ^c ctc ccc cag gg ^c ccc Gly Ser Phe Leu Thr Ser Leu Leu Lys Lys Gly Leu Pro Gln Ala Pro	1829
584 589 594 599	
agc tga ggccggcaac tcacccagcc gccacctctg ccctctccca gctggacaga Ser *	1885
600	
ccctgggcct gcacttcagg actgtgggtg ccctgggtga acagaccctg caggtcccat	1945
ccctggggac agaggccttg tgtcacctgc ctgcccaggc agctgtttgc agctgaagaa	2005
acaaaactggc tccaggctg tcttgccctt attcctggtt agggcagg ^t g gtcctagaca	2065
gcagtttcca gtaaaagctg aacaaaaaaaaaaaa	2100

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 <211> 657
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 <213> Homo sapiens

<220>

<221> CDS

<222> (40)..(453)

<400> 543

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	Met Thr Ser His Ala	
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cgc gta cgt aag ctt gga tcc tct aga gcg gcc cta cta cta cta aat		102
Arg Val Arg Lys Leu Gly Ser Ser Arg Ala Ala Leu Leu Leu Asn		
6 11 16 21		
tcg cgg ccg cgt cga cca aaa atg gcg gta gtt ggt gtg tcc tcg gtt		150
Ser Arg Pro Arg Arg Pro Lys Met Ala Val Val Gly Val Ser Ser Val		
22 27 32 37		
tct cgg ctg ctg ggt cgg tcc cgc cca cag ctg ggg cgg cct atg tcg		198
Ser Arg Leu Leu Gly Arg Ser Arg Pro Gln Leu Gly Arg Pro Met Ser		
38 43 48 53		
agt ggc gcc cat ggc gaa gag ggc tca gct cgc atg tgg aag act ctc		246
Ser Gly Ala His Gly Glu Gly Ser Ala Arg Met Trp Lys Thr Leu		
54 59 64 69		
acc ttc ttc gtc gcg ctc ccc ggg gtg gca gtc agc atg ctg aat gtg		294
Thr Phe Phe Val Ala Leu Pro Gly Val Ala Val Ser Met Leu Asn Val		
70 75 80 85		
tac ctg aag tcg cac cac gga gag cac gag aga ccc gag ttc atc gcc		342
Tyr Leu Lys Ser His His Gly Glu His Glu Arg Pro Glu Phe Ile Ala		
86 91 96 101		
tac ccc cat ctc cgc atc agg acc aag ccg ttt ccc tgg gga gat ggt		390
Tyr Pro His Leu Arg Ile Arg Thr Lys Pro Phe Pro Trp Gly Asp Gly		
102 107 112 117		
aac cat act cta ttc cat aac cct cat gtg aat cca ctt cca act ggc		438
Asn His Thr Leu Phe His Asn Pro His Val Asn Pro Leu Pro Thr Gly		
118 123 128 133		
tac gaa gat gaa taa agagaatctg gaccactacc cgggcaccag ggaccacagc		493
Tyr Glu Asp Glu *		
134		
actggtttgg accgttactc tgcacatgga ccagaaaaag tatatggac cttaagctca		553
ccttctttac ttgtatcaaa tgatgactgg tatactggc tcccatccct ttgcttgtgg		613
caggagatgg cttaaataaa taacttaaac ttaaaaaaaaaaa aaaa		657

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<211> 1505

<212> DNA

<213> Homo sapiens

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Met Glu Val Lys Pro Pro Pro Gly Arg Pro Gln Pro Asp
1 5 10
tcc ggc cgt cgc cgt cgc cgg ggg gag gag ggc cat gat cca aag 158
Ser Gly Arg Arg Arg Arg Arg Gly Glu Glu Gly His Asp Pro Lys
14 19 24 29
gaa cca gag cag ttg aga aaa ctg ttt att ggt ggt ctg agc ttt gaa 206
Glu Pro Glu Gln Leu Arg Lys Leu Phe Ile Gly Gly Leu Ser Phe Glu
30 35 40 45
act aca gat gat agt tta cga gaa cat ttt gag aaa tgg ggc aca ctc 254
Thr Thr Asp Asp Ser Leu Arg Glu His Phe Glu Lys Trp Gly Thr Leu
46 51 56 61
aca gat tgt gtg gta atg aga gac ccc caa aca aaa cgt tcc agg ggc 302
Thr Asp Cys Val Val Met Arg Asp Pro Gln Thr Lys Arg Ser Arg Gly
62 67 72 77
ttt ggt ttt gtg act tat tct tgt gtt gaa gag gtg gat gca gca atg 350
Phe Gly Phe Val Thr Tyr Ser Cys Val Glu Glu Val Asp Ala Ala Met
78 83 88 93
tgt gct cga cca cac aag gtt gat ggg cgt gta gtg gaa cca aag aga 398
Cys Ala Arg Pro His Lys Val Asp Gly Arg Val Val Glu Pro Lys Arg
94 99 104 109
gct gtt tct aga gag gat tct gta aag cct ggt gcc cat cta aca gtg 446
Ala Val Ser Arg Glu Asp Ser Val Lys Pro Gly Ala His Leu Thr Val
110 115 120 125
aag aaa att ttt gtt ggt att aaa gaa gat aca gaa gaa tat aat 494
Lys Lys Ile Phe Val Gly Gly Ile Lys Glu Asp Thr Glu Glu Tyr Asn
126 131 136 141
ttg aga gac tac ttt gaa aag tat ggc aag att gaa acc ata gaa gtt 542
Leu Arg Asp Tyr Phe Glu Lys Tyr Gly Lys Ile Glu Thr Ile Glu Val
142 147 152 157
atg gaa gac agg cag agt gga aaa aag aga gga ttt gct ttt gta act 590
Met Glu Asp Arg Gln Ser Gly Lys Lys Arg Gly Phe Ala Phe Val Thr
158 163 168 173
| ttt gat gat cat gat aca gtt gat aaa att gtt gtt cag aaa tac cac 638
/ Phe Asp Asp His Asp Thr Val Asp Lys Ile Val Val Gln Lys Tyr His
174 179 184 189
act att aat ggg cat aat tgt gaa gtg aaa aag gcc ctt tct aaa caa 686

Thr Ile Asn Gly His Asn Cys Glu Val Lys Lys Ala Leu Ser Lys Gln			
190	195	200	205
gag atg cag tct gct gga tca cag aga ggt cgt gga ggt gga tct ggc			734
Glu Met Gln Ser Ala Gly Ser Gln Arg Gly Arg Gly Gly Ser Gly			
206	211	216	221
aat ttt atg ggt cgc gga ggg aac ttt gga ggt ggt gga ggt aat ttt			782
Asn Phe Met Gly Arg Gly Asn Phe Gly Gly Gly Gly Asn Phe			
222	227	232	237
ggc cgt ggt gga aac ttt ggt gga aga gga ggc tat ggt ggt gga ggt			830
Gly Arg Gly Gly Asn Phe Gly Gly Arg Gly Gly Tyr Gly Gly Gly			
238	243	248	253
ggt ggc agc aga ggt agt tat gga gga ggt gat ggt gga tat aat gga			878
Gly Gly Ser Arg Gly Ser Tyr Gly Gly Asp Gly Gly Tyr Asn Gly			
254	259	264	269
ttt gga ggt gat ggt ggc aac tat ggc ggt ggt cct ggt tat agt agt			926
Phe Gly Gly Asp Gly Gly Asn Tyr Gly Gly Pro Gly Tyr Ser Ser			
270	275	280	285
aga ggg ggc tat ggt ggt gga cca gga tat gga aac caa ggt ggt			974
Arg Gly Gly Tyr Gly Gly Pro Gly Tyr Gly Asn Gln Gly Gly			
286	291	296	301
gga tat ggt gga ggt gga gga tat gat ggt tac aat gaa gga gga aat			1022
Gly Tyr Gly Gly Tyr Asp Gly Tyr Asn Glu Gly Gly Asn			
302	307	312	317
ttt ggc ggt ggt aac tat ggt ggt ggg aac tat aat gat ttt gga			1070
Phe Gly Gly Asn Tyr Gly Gly Asn Tyr Asn Asp Phe Gly			
318	323	328	333
aat tat agt gga caa cag caa tca aat tat gga ccc atg aaa ggg ggc			1118
Asn Tyr Ser Gly Gln Gln Ser Asn Tyr Gly Pro Met Lys Gly Gly			
334	339	344	349
agt ttt ggt gga aga agc tcg ggc agt ccc tat ggt ggt ggt tat gga			1166
Ser Phe Gly Gly Arg Ser Ser Gly Ser Pro Tyr Gly Gly Tyr Gly			
350	355	360	365
tct ggt ggt gga agt ggt gga tat ggt agc aga agg ttc taa aaacagc			1215
Ser Gly Gly Ser Gly Gly Tyr Gly Ser Arg Arg Phe *			
366	371	376	
agaaaagggc tacagttctt agcaggagag agagcgagga gttgtcagga aagctgcagg			1275
ttactttgag acagtcgtcc caaatgcatt agaggaactg taaaaatctg ccacagaagg			1335
aacgatgatc catagtcaga aaagttactg cagcttaaac aggaaccctt cttgttcagg			1395
actgtcatag ccacagttt caaaagtgc a gctattgatt aatgcatgta gtgtcaatta			1455
gatgtcaatc ctgaggcttt tatctgttgc gcttcctt tcctttcctt			1505

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 <222> (168)..(542)

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 gaaaccccaag gcgtggagat tgatcctgcg agagaagggg gttcatc atg gcg gat 176
 Met Ala Asp
 1

 gac cta aag cga ttc ttg tat aaa aag tta cca agt gtt gaa ggg ctc 224
 Asp Leu Lys Arg Phe Leu Tyr Lys Lys Leu Pro Ser Val Glu Gly Leu
 4 9 14 19

 cat gcc att gtt gtg tca gat aga gat gga gta cct gtt att aaa gtg 272
 His Ala Ile Val Val Ser Asp Arg Asp Gly Val Pro Val Ile Lys Val
 20 25 30 35

 gca aat gac aat gct cca gag cat gct ttg cga cct ggt ttc tta tcc 320
 Ala Asn Asp Asn Ala Pro Glu His Ala Leu Arg Pro Gly Phe Leu Ser
 36 41 46 51

 act ttt gcc ctt gca aca gac caa gga agc aaa ctt gga ctt tcc aaa 368
 Thr Phe Ala Leu Ala Thr Asp Gln Gly Ser Lys Leu Gly Leu Ser Lys
 52 57 62 67

 aat aaa agt atc atc tgt tac tat aac acc tac cag gtg gtt caa ttt 416
 Asn Lys Ser Ile Ile Cys Tyr Tyr Asn Thr Tyr Gln Val Val Gln Phe
 68 73 78 83

 aat cgt tta cct ttg gtg gtg agt ttc ata gcc agc agc agt gcc aat 464
 Asn Arg Leu Pro Leu Val Val Ser Phe Ile Ala Ser Ser Ser Ala Asn
 84 89 94 99

 aca gga cta att gtc agc cta gaa aag gaa ctt gct cca ttg ttt gaa 512
 Thr Gly Leu Ile Val Ser Leu Glu Lys Glu Leu Ala Pro Leu Phe Glu
 100 105 110 115

 gaa ctg aga caa gtt gtg gaa gtt tct taa t ctgacagtgg tttcagtgtg 563
 Glu Leu Arg Gln Val Val Glu Val Ser *
 116 121

 taccttatct tcattataac aacacaatat caatccagca atcttttagac tacaataata 623
 cttttatcca tggctcaag aaagggcccc ttttccaac ttatactaaa gagcttagcat 683

atagatgtaa tttatagata gatcagttgc tatattttct ggtgtagggt ctttcttatt	743
tagtgagatc tagggatacc acagaaatgg ttcagtctat cacagctccc atggagttag	803
tctggtcacc agatatggat gagagattct attcagtgga tcagaatcaa actggtacat	863
tgatccactt gagccgttaa gtgctgccaa ttgtacaata tgcccaggct tgcagaataa	923
agccaaacttt ttattgtgaa taataataag gacatatttt tcttcagatt atgttttatt	983
tcttcgcatt gagtgaggaa cataaaatgg cttggtaaaa gtaataaaat cagtacaatc	1043
actaactttc ctttgacat attattttgc agtatacatg aatattacta atcagttga	1103
ttattctcag agggtgctgc tcttaatga aaatgaaaat tatagcta at gtttttcct	1163
caaactctgc tttctgtaac caatcagtgt tttaatgttt gtgtgttctt cataaaattt	1223
aaatacaatt cgttattctg tttccaatgt tagtatgtat gtaaacatga tagtacagcc	1283
attttttca tatgtgagta aaaataaaat agtattttta aaaatatagt ttgagcactg	1343
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tcagccacat gaataaataa tgagtgttcc ttgtaaa	1440

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 <212> DNA
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Met Ala Ser Ala Gly Gly	
1	
gaa gac tgc gag agc ccc gcg ccg gag gcc gac cgt ccg cac cag cgg	160
Glu Asp Cys Glu Ser Pro Ala Pro Glu Ala Asp Arg Pro His Gln Arg	
7 12 17 22	
ccc ttc ctg ata ggg gtg agc ggc act gcc agc ggg aag tcg acc	208
Pro Phe Leu Ile Gly Val Ser Gly Gly Thr Ala Ser Gly Lys Ser Thr	
23 28 33 38	
gtg tgt gag aag atc atg gag ttg ctg gga cag aac gag gtg gaa cag	256
Val Cys Glu Lys Ile Met Glu Leu Leu Gly Gln Asn Glu Val Glu Gln	
39 44 49 54	

cgg cag cgg aag gtg gtc atc ctg agc cag gac agg ttc tac aag gtc		304
Arg Gln Arg Lys Val Val Ile Leu Ser Gln Asp Arg Phe Tyr Lys Val		
55 60 65 70		
ctg acg gca gag cag aag gcc aag gcc ttg aaa gga cag tac aat ttt		352
Leu Thr Ala Glu Gln Lys Ala Lys Ala Leu Lys Gly Gln Tyr Asn Phe		
71 76 81 86		
gac cat cca gat gcc ttt gat aat gat ttg atg cac agg act ctg aag		400
Asp His Pro Asp Ala Phe Asp Asn Asp Leu Met His Arg Thr Leu Lys		
87 92 97 102		
aac atc gtg gag ggc aaa acg gtg gag gtg ccg ace tat gat ttt gtg		448
Asn Ile Val Glu Gly Lys Thr Val Glu Val Pro Thr Tyr Asp Phe Val		
103 108 113 118		
aca cac tca agg tta cca gag acc acg gtg gtc tac cct gcg gac gtg		496
Thr His Ser Arg Leu Pro Glu Thr Thr Val Val Tyr Pro Ala Asp Val		
119 124 129 134		
gtt ctg ttt gag ggc atc ttg gtg ttc tac agc cag gag atc cgg gac		544
Val Leu Phe Glu Gly Ile Leu Val Phe Tyr Ser Gln Glu Ile Arg Asp		
135 140 145 150		
atg ttc cac ctg cgc ctc ttc gtg gac acc gac tcc gac gtc agg ctg		592
Met Phe His Leu Arg Leu Phe Val Asp Thr Asp Ser Asp Val Arg Leu		
151 156 161 166		
tct cga aga gtt ctc cgg gac gtg cgc cga ggg agg gac ctg gag cag		640
Ser Arg Arg Val Leu Arg Asp Val Arg Arg Gly Arg Asp Leu Glu Gln		
167 172 177 182		
att ctg acg cag tac acc acc ttc gtg aag ccg gcc ttc gag gag ttc		688
Ile Leu Thr Gln Tyr Thr Phe Val Lys Pro Ala Phe Glu Glu Phe		
183 188 193 198		
tgc ctg ccg aca aag aag tat gcc gat gtg atc atc cca cga gga gtg		736
Cys Leu Pro Thr Lys Lys Tyr Ala Asp Val Ile Ile Pro Arg Gly Val		
199 204 209 214		
gac aat atg gtt gcc atc aac ctg atc gtg cag cac atc cag gac att		784
Asp Asn Met Val Ala Ile Asn Leu Ile Val Gln His Ile Gln Asp Ile		
215 220 225 230		
ctg aat ggt gac atc tgc aaa tgg cac cga gga ggg tcc aat ggg cgg		832
Leu Asn Gly Asp Ile Cys Lys Trp His Arg Gly Gly Ser Asn Gly Arg		
231 236 241 246		
agc tac aag cgg acc ttt tct gag cca ggg gac cac cct ggg atg ctg		880
Ser Tyr Lys Arg Thr Phe Ser Glu Pro Gly Asp His Pro Gly Met Leu		
247 252 257 262		
acc tct ggc aaa cgg tca cat ttg gag tcc agc agc aga ccc cac tga		928
Thr Ser Gly Lys Arg Ser His Leu Glu Ser Ser Ser Arg Pro His *		
263 268 273 278		
ggggctgccc agcctcaggg caggtctccc gccccatg tgtgttcagg aactgagcct		988

ggggacgccc acccacaccc actgctatgt ggagctcaca gcctcacatg tgaacacccg	1048
tgtctgggtt gcctggggtg atcctccctc ctgcgtggtg gctgtctctg gaaagcatcc	1108
cttgcgcgtg ccacgggcag ccccagcccc cgtccgtcca ggctcaccca cagtagtgat	1168
gcagacgtga cgtgggggaa gggggctgag ccctgtggct gggttctgac aactgtaaacg	1228
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<210> 547
<211> 2670
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (107) .. (634)

<400> 547

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acagctgaag gctgcgaggg actaagagca gaatataatct tttagaa atg agt tgc 115
Met Ser Cys
1

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aca att gag aag gca ctt gcc gac gct aaa gct ctt gtt gaa aga tta      163
Thr Ile Glu Lys Ala Leu Ala Asp Ala Lys Ala Leu Val Glu Arg Leu
4          9          14          19

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  aga gat cat gac gat gca gca gaa tct ctg att gag caa acc aca gct      211
  Arg Asp His Asp Asp Ala Ala Glu Ser Leu Ile Glu Gln Thr Thr Ala
  20          25          30          35

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ctc aac aag cga gta gaa gcc atg aaa cag tat cag gaa gaa att caa 259
 Leu Asn Lys Arg Val Glu Ala Met Lys Gln Tyr Gln Glu Glu Ile Gln
 36 41 46 51

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gaa ctt aat gaa gtc gcg aga cat cgg cca cgg tcc acg tta gtt atg 307
Glu Leu Asn Glu Val Ala Arg His Arg Pro Arg Ser Thr Leu Val Met
 52           57           62           67

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gga atc cag caa gaa aac aga caa atc aga gag ttg caa caa gaa aac 355
 Gly Ile Gln Gln Glu Asn Arg Gln Ile Arg Glu Leu Gln Gln Glu Asn
 68 73 78 83

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aaa gaa tta cgt aca tct ctg gaa gaa cat cag tcg gcc ttg gaa ctt      403
Lys Glu Leu Arg Thr Ser Leu Glu Glu His Gln Ser Ala Leu Glu Leu
 84           89           94           99

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ata atg agc aag tac cga gaa caa atg ttt aga ttg cta atg gct agc      451
Ile Met Ser Lys Tyr Arg Glu Gln Met Phe Arg Leu Leu Met Ala Ser
100          105                  110          115

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aaa aaa gat gat ccg ggt ata ata atg aag tta aaa gag cag cac tcc	499
Lys Lys Asp Asp Pro Gly Ile Ile Met Lys Leu Lys Glu Gln His Ser	
116 121 126 131	
aag gaa ctg caa gca cat gtt gac cag ata act gaa atg gca gca gta	547
Lys Glu Leu Gln Ala His Val Asp Gln Ile Thr Glu Met Ala Ala Val	
132 137 142 147	
atg agg aag cca ttg aaa ttg acg agc aac agg gtt gca agg aac aag	595
Met Arg Lys Pro Leu Lys Leu Thr Ser Asn Arg Val Ala Arg Asn Lys	
148 153 158 163	
aac gaa tat ttc aac ttg aac aag aaa aca aag gct tga gagagatcct	644
Asn Glu Tyr Phe Asn Leu Asn Lys Lys Thr Lys Ala *	
164 169 174	
tcaaataact cgagaatcat ttttgaacct aagggaaagat gatgcgtcgg aaagtacttc	704
tttgcagca ttagtgacca acagtgattt gagtctgagg aagagctgaa gagtttctga	764
gtctgtgagc ttcttacatg gctccaaatg gtcaaataag tgaatgaatg aatggacaga	824
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aacaaaaaaat gcatagttaa tggcataga ctttattcca aaacataatt ggaaaataga	944
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ccaaagagctt ttggcagtac tgctggctt ctgggtgatt aatttagttaa acttgaatata	1064
tcccagtaaa tgtttgagaa tgcataaaat tataccaatt taaaaatata aattttgcc	1124
actgtttgt gaacggagga tttgtacgct aaatttcatac cttatggc gtcaaagttg	1184
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gataatttaa ttttagcaat ttatcataac tgatacttag ctaacaattt tccataactt	1364
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ctgaaagtgg gggtaaaggt ggagtaatct gtggatttgt ttctgttgc ttttaaaatg	1844

tcaaatatat aatatgtaat	ttttttaaaa accaccagat acagaaatgt	gctttaacat	1904
cagttgaaac ctaaatttc ttatgttgc	gtgattgtat taaaaggaa taaaagaaga		1964
gtgtcaaaca tggtaaata tattgtactc	atttatgttgc aatacgtatt aaaattaaga		2024
caagtggaaa attatacttt gagtatataa	ttgtttaat attactttat atggtaattt		2084
tatgtataat ttcatatatt ggtaaaattc	aaaactacac ttgagaattt ttttatctta		2144
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agtttttatt tttaaacttt ttattgttt	tggaaagta ttcccttaatt taatgacaca		2324
ttcattcaga tacttcttat ccctgcta	aaaggaaatc tatttcaagc tacaccattt		2384
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taaggtcttc atgtttaaag acatttactt	tgttatttttag tgacacattt ccacccattt		2564
ttttttttt ttttgggtt ttgttaaaca	gaaccttaag tttatgttttgc aggtatgtac		2624
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 <211> 1764
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (365)..(916)

<400> 548

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agtgagtgtat ggatttggAAC	tgagaccgaa atataatggaa attttacatt gcttgcatt	180
catttggaaa cttgatggac tacggggact	ttatcaagga gtaaccccaa atatatgggg	240
tgcaggttta tcctgggac tctactttt	ctttacaat gccatcaagt catataaaac	300
agaaggaaga gctgaacgtt tagaggcaac	agaatacctt gtctcagctg ctgaagctgg	360
agcc atg acc ctc tgc att aca aac cca tta tgg gta aca aaa act cgc		409
Met Thr Leu Cys Ile Thr Asn Pro Leu Trp Val Thr Lys Thr Arg		
1	5	10

ctt atg tta cag tat gat gct gtt aac tcc cca cac cga caa tat Leu Met Leu Gln Tyr Asp Ala Val Val Asn Ser Pro His Arg Gln Tyr 16 21 26 31	457
aaa gga atg ttt gat aca ctt gtg aaa ata tat aag tat gaa ggt gtg Lys Gly Met Phe Asp Thr Leu Val Lys Ile Tyr Lys Tyr Glu Gly Val 32 37 42 47	505
cgt gga tta tat aag gga ttt gtt cct ggg ctg ttt gga aca tcg cat Arg Gly Leu Tyr Lys Gly Phe Val Pro Gly Leu Phe Gly Thr Ser His 48 53 58 63	553
ggt gcc ctt cag ttt atg gca tat gaa ttg ctg aag ttg aag tac aac Gly Ala Leu Gln Phe Met Ala Tyr Glu Leu Leu Lys Leu Lys Tyr Asn 64 69 74 79	601
cag cat atc aat aga tta cca gaa gcc cag ttg agc aca gta gaa tat Gln His Ile Asn Arg Leu Pro Glu Ala Gln Leu Ser Thr Val Glu Tyr 80 85 90 95	649
ata tct gtt gca gca cta tcc aaa ata ttt gct gtc gca gca aca tac Ile Ser Val Ala Ala Leu Ser Lys Ile Phe Ala Val Ala Ala Thr Tyr 96 101 106 111	697
cca tat caa gtc gta aga gct cgt ctt cag gat caa cac atg ttt tac Pro Tyr Gln Val Val Arg Ala Arg Leu Gln Asp Gln His Met Phe Tyr 112 117 122 127	745
agt ggt gta ata gat gta atc aca aag aca tgg agg aaa gaa ggc gtc Ser Gly Val Ile Asp Val Ile Thr Lys Thr Trp Arg Lys Glu Gly Val 128 133 138 143	793
ggt gga ttt tac aag gga att gct cct aat ttg att aga gtg act cca Gly Gly Phe Tyr Lys Gly Ile Ala Pro Asn Leu Ile Arg Val Thr Pro 144 149 154 159	841
gcc tgc tgt att acc ttt gtg gta tat gaa aac gtc tca cat ttt tta Ala Cys Cys Ile Thr Phe Val Val Tyr Glu Asn Val Ser His Phe Leu 160 165 170 175	889
ctt gac ctt aga gaa aag aga aag taa gctca aagaggacaa ttccagtata Leu Asp Leu Arg Glu Lys Arg Lys *176 181	941
tctgcccaag gcagcaacaa gcttttgt gtttaaggca taaaagaaga attctgcata gaaacatggc tcatattcga aattgctcta tagtcattag aagccagaga actgctaagt ctcctgcaat gttttctgc ttttgcctt cccatatat atgaaacttg gctacctctg cctgaaatgg ctgccatcaa cacaatgtta aaactgacac gaagtataga gtttcacaga tttctacgtt ttattgggtgg aagctgattt gcaacatttg ctaaatggat tagatgaatg tacttctttt tgtgagctta cttgcctgga ttgcattaaa attaaccttt gtgcaataacc aagaaaatag ctcttaaaa gaatgtctt gtatgtctca aggtaaattha aggattact	1001 1061 1121 1181 1241 1301 1361

gaataaggtg ttgaccaaattt ccagaccatt ttattttattt tttttattta tttatttttt	1421
gagatggagt cttgcattgt cggccaggct ggagtgcagt ggcgtgatct cagctcactg	1481
caacccctccac ctccccgggtt cacgccattc tcctgcctca gcctcctgag tagctgggac	1541
tacaggcacc tgccaccacg cctggctaac tttttttat attttgagta gaaatggggt	1601
ttcaccatgt tagccaggat gggctcaatc tcctgacctt gtgatccgccc tgccttggcc	1661
tcccaaagtg ctgggattac aggcggtgagc cactgcgcct ggccagacca ttttagaatt	1721
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		1		
cgc gag ctg cgg gcg ctg ctg tgg ggc cgc cgc ctg cgg cct ttg				103
Arg Glu Leu Arg Ala Leu Leu Trp Gly Arg Arg Leu Arg Pro Leu				
3 8 13 18				
ctg cgg cgc gcg ctg gcg gcc gtg ccg gga gga aaa cca att ctg				151
Leu Arg Ala Pro Ala Leu Ala Ala Val Pro Gly Gly Lys Pro Ile Leu				
19 24 29 34				
tgt cct cgg agg acc aca gcc cag ttg ggc ccc agg cga aac cca gcc				199
Cys Pro Arg Arg Thr Thr Ala Gln Leu Gly Pro Arg Arg Asn Pro Ala				
35 40 45 50				
tgg agc ttg cag gca gga cga ctg ttc agc acg cag acc gcc gag gac				247
Trp Ser Leu Gln Ala Gly Arg Leu Phe Ser Thr Gln Thr Ala Glu Asp				
51 56 61 66				
aag gag gaa ccc ctg cac tcg att atc agc agc aca gag agc gtg cag				295
Lys Glu Glu Pro Leu His Ser Ile Ile Ser Ser Thr Glu Ser Val Gln				
67 72 77 82				
ggc tcc act tcc aaa cat gag ttc cag gcc gag aca aag aag ctt ttg				343
Gly Ser Thr Ser Lys His Glu Phe Gln Ala Glu Thr Lys Lys Leu Leu				
83 88 93 98				
gac att gtt gcc cgg tcc ctg tac tca gaa aaa gag gtg ttt ata cgg				391

Asp Ile Val Ala Arg Ser Leu Tyr Ser Glu Lys Glu Val Phe Ile Arg				
99	104	109	114	
gag ctg atc tcc aat gcc agc gat gcc ttg gaa aaa ctg cgt cac aaa				439
Glu Leu Ile Ser Asn Ala Ser Asp Ala Leu Glu Lys Leu Arg His Lys				
115	120	125	130	
ctg gtg tct gac ggc caa gca ctg cca gaa atg gag att cac ttg cag				487
Leu Val Ser Asp Gly Gln Ala Leu Pro Glu Met Glu Ile His Leu Gln				
131	136	141	146	
acc aat gcc gag aaa ggc acc atc acc atc cag gat act ggt atc ggg				535
Thr Asn Ala Glu Lys Gly Thr Ile Thr Ile Gln Asp Thr Gly Ile Gly				
147	152	157	162	
atg aca cag gaa gag ctg gtg tcc aac ctg ggg acg att gcc aga tcg				583
Met Thr Gln Glu Leu Val Ser Asn Leu Gly Thr Ile Ala Arg Ser				
163	168	173	178	
ggg tca aag gcc ttc ctg gat gct ctg cag aac cag gct gag gcc agc				631
Gly Ser Lys Ala Phe Leu Asp Ala Leu Gln Asn Gln Ala Glu Ala Ser				
179	184	189	194	
agc aag atc atc ggc cag ttt gga gtg ggt ttc tac tca gct ttc atg				679
Ser Lys Ile Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser Ala Phe Met				
195	200	205	210	
gtg gct gac aga gtg gag gtc tat tcc cgc tcg gca gcc ccg ggg agc				727
Val Ala Asp Arg Val Glu Val Tyr Ser Arg Ser Ala Ala Pro Gly Ser				
211	216	221	226	
ctg ggt tac cag tgg ctt tca gat ggt tct gga gtg ttt gaa atc gcc				775
Leu Gly Tyr Gln Trp Leu Ser Asp Gly Ser Gly Val Phe Glu Ile Ala				
227	232	237	242	
gaa gct tcg gga gtt aga acc ggg aca aaa atc atc atc cac ctg aaa				823
Glu Ala Ser Gly Val Arg Thr Gly Thr Lys Ile Ile Ile His Leu Lys				
243	248	253	258	
tcc gac tgc aag gag ttt tcc agc gag gcc cgg gtg cga gat gtg gta				871
Ser Asp Cys Lys Glu Phe Ser Ser Glu Ala Arg Val Arg Asp Val Val				
259	264	269	274	
acg aag tac agc aac ttc gtc agc ttc ccc ttg tac ttg aat gga agg				919
Thr Lys Tyr Ser Asn Phe Val Ser Phe Pro Leu Tyr Leu Asn Gly Arg				
275	280	285	290	
cggtt gac aac acc ttg cag gcc atc tgg atg atg gac ccc aag gat gtc				967
Arg Met Asn Thr Leu Gln Ala Ile Trp Met Met Asp Pro Lys Asp Val				
291	296	301	306	
cgt gag tgg caa cat gag gag ttc tac cgc tac gtc gcg cag gct cac				1015
Arg Glu Trp Gln His Glu Glu Phe Tyr Arg Tyr Val Ala Gln Ala His				
307	312	317	322	
gac aag ccc cgc tac acc ctg cac tat aag acg gac gca ccg ctc aac				1063
Asp Lys Pro Arg Tyr Thr Leu His Tyr Lys Thr Asp Ala Pro Leu Asn				

323	328	333	338	
atc cgc agc atc ttc tac gtg ccc gac atg aaa ccg tcc atg ttt gat Ile Arg Ser Ile Phe Tyr Val Pro Asp Met Lys Pro Ser Met Phe Asp				1111
339	344	349	354	
gtg agc cgg gag ctg ggc tcc agc gtt gca ctg tac agc cgc aaa gtc Val Ser Arg Glu Leu Gly Ser Ser Val Ala Leu Tyr Ser Arg Lys Val				1159
355	360	365	370	
ctc atc cag acc aag gcc acg gac atc ctg ccc aag tgg ctg cgc ttc Leu Ile Gln Thr Lys Ala Thr Asp Ile Leu Pro Lys Trp Leu Arg Phe				1207
371	376	381	386	
atc cga ggt gtg gtg gac agt gag gac att ccc ctg aac ctc agc cgg Ile Arg Gly Val Val Asp Ser Glu Asp Ile Pro Leu Asn Leu Ser Arg				1255
387	392	397	402	
gag ctg ctg cag gag agc gca ctc atc agg aaa ctc cgg gac gtt tta Glu Leu Leu Gln Glu Ser Ala Leu Ile Arg Lys Leu Arg Asp Val Leu				1303
403	408	413	418	
cag cag agg ctg atc aaa ttc ttc att gac cag agt aaa aaa gat gct Gln Gln Arg Leu Ile Lys Phe Phe Ile Asp Gln Ser Lys Lys Asp Ala				1351
419	424	429	434	
gag aag tat gca aag ttt ttt gaa gat tac ggc ctg ttc atg cgg gag Glu Lys Tyr Ala Lys Phe Phe Glu Asp Tyr Gly Leu Phe Met Arg Glu				1399
435	440	445	450	
ggc att gtg acc gcc acc gag cag gag gtc aag gag gac ata gca aag Gly Ile Val Thr Ala Thr Glu Gln Glu Val Lys Glu Asp Ile Ala Lys				1447
451	456	461	466	
ctg ctg cgc tac gag tcc tcg gcg ctg ccc tcc ggg cag cta acc agc Leu Leu Arg Tyr Glu Ser Ser Ala Leu Pro Ser Gly Gln Leu Thr Ser				1495
467	472	477	482	
ctc tca gaa tac gcc agc cgc atg cgg gcc ggc acc cgc aac atc tac Leu Ser Glu Tyr Ala Ser Arg Met Arg Ala Gly Thr Arg Asn Ile Tyr				1543
483	488	493	498	
tac ctg tgc gcc ccc aac cgt cac ctg gca gag cac tca ccc tac tat Tyr Leu Cys Ala Pro Asn Arg His Leu Ala Glu His Ser Pro Tyr Tyr				1591
499	504	509	514	
gag gcc atg aag aag aaa gac aca gag gtt ctc ttc tgc ttt gag cag Glu Ala Met Lys Lys Asp Thr Glu Val Leu Phe Cys Phe Glu Gln				1639
515	520	525	530	
ttt gat gag ctc acc ctg ctg cac ctt cgt gag ttt gac aag aag aag Phe Asp Glu Leu Thr Leu Leu His Leu Arg Glu Phe Asp Lys Lys Lys				1687
531	536	541	546	
ctg atc tct gtg gag acg gac ata gtc gtg gat cac tac aag gag gag Leu Ile Ser Val Glu Thr Asp Ile Val Val Asp His Tyr Lys Glu Glu				1735
547	552	557	562	

aag ttt gag gac agg tcc cca gcc gcc gag tgc cta tca gag aag gag	1783
Lys Phe Glu Asp Arg Ser Pro Ala Ala Glu Cys Leu Ser Glu Lys Glu	
563 568 573 578	
acg gag gag ctc atg gcc tgg atg aga aat gtg ctg ggg tcg cgt gtc	1831
Thr Glu Glu Leu Met Ala Trp Met Arg Asn Val Leu Gly Ser Arg Val	
579 584 589 594	
acc aac gtg aag gtg acc ctc cga ctg gac acc cac cct gcc atg gtc	1879
Thr Asn Val Lys Val Thr Leu Arg Leu Asp Thr His Pro Ala Met Val	
595 600 605 610	
acc gtg ctg gag atg ggg gct gcc cgc cac ttc ctg cgc atg cag cag	1927
Thr Val Leu Glu Met Gly Ala Ala Arg His Phe Leu Arg Met Gln Gln	
611 616 621 626	
ctg gcc aag acc cag gag gag cgc gca cag ctc ctg cag ccc acg ctg	1975
Leu Ala Lys Thr Gln Glu Glu Arg Ala Gln Leu Leu Gln Pro Thr Leu	
627 632 637 642	
gag atc aac ccc agg cac gcg ctc atc aag aag ctg aat cag ctg cgc	2023
Glu Ile Asn Pro Arg His Ala Leu Ile Lys Lys Leu Asn Gln Leu Arg	
643 648 653 658	
gca agc gag cct ggc ctg gct cag ctg ctg gtg gat cag ata tac gag	2071
Ala Ser Glu Pro Gly Leu Ala Gln Leu Leu Val Asp Gln Ile Tyr Glu	
659 664 669 674	
aac gcc atg att gct gct gga ctt gtt gac gac cct agg gcc atg gtg	2119
Asn Ala Met Ile Ala Ala Gly Leu Val Asp Asp Pro Arg Ala Met Val	
675 680 685 690	
ggc cgc ttg aat gag ctg ctt gtc aag gcc ctg gag cga cac tga cag	2167
Gly Arg Leu Asn Glu Leu Leu Val Lys Ala Leu Glu Arg His *	
691 696 701	
ccagggggcc agaaggactg acaccacaga tgacagcccc acctccttga gctttattha	2227
cctaaattta aaggtatttc ttaacccgag tgtgtgttgg gcttttttc tgggtcctgt	2287
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gcatcacccct cactggatag tggtcactga tggcttggc tgcaggcaag tgggcacagg	2407
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<220>
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acc atg gcc ggc atg gtg gac ttc cag gat gag gag cag gtc aag tcc 108
Met Ala Gly Met Val Asp Phe Gln Asp Glu Glu Gln Val Lys Ser
1 5 10

ttt ttg gag aac atg gag gtg gag tgc aac tac cac tgc tac cac gag 156
Phe Leu Glu Asn Met Glu Val Glu Cys Asn Tyr His Cys Tyr His Glu
16 21 26 31

aag gac ccg gac ggt tgc tat cgg ctg gtg gac tat ttg gaa ggg atc 204
Lys Asp Pro Asp Gly Cys Tyr Arg Leu Val Asp Tyr Leu Glu Gly Ile
32 37 42 47

cgg aag aat ttt gat gag gct gcc aag gtg ttg aag ttt aac tgt gaa 252
Arg Lys Asn Phe Asp Glu Ala Ala Lys Val Leu Lys Phe Asn Cys Glu
48 53 58 63

gag aac cag cac agt gat agc tgc tac aaa ctg ggg gcc tac tat gtg 300
Glu Asn Gln His Ser Asp Ser Cys Tyr Lys Leu Gly Ala Tyr Tyr Val
64 69 74 79

act gga aaa ggt ggt ctg acc cag gac ctg aaa gct gcc gcc agg tgc 348
Thr Gly Lys Gly Leu Thr Gln Asp Leu Lys Ala Ala Ala Arg Cys
80 85 90 95

ttt ttg atg gcg tgt gag aag cct gga aag aag tca ata gca gca tgt 396
Phe Leu Met Ala Cys Glu Lys Pro Gly Lys Lys Ser Ile Ala Ala Cys
96 101 106 111

cac aac gtt ggc ctc ctg gca cat gat gga cag gtt aat gag gat ggc 444
His Asn Val Gly Leu Leu Ala His Asp Gly Gln Val Asn Glu Asp Gly
112 117 122 127

cag cct gac ttg gga aag gcc agg gac tac tac aca agg gcc tgt gat 492
Gln Pro Asp Leu Gly Lys Ala Arg Asp Tyr Tyr Thr Arg Ala Cys Asp
128 133 138 143

ggc tat act tcc agt tgc ttc aac ctc agt gcc atg ttc ctg cag 540
Gly Gly Tyr Thr Ser Ser Cys Phe Asn Leu Ser Ala Met Phe Leu Gln
144 149 154 159

ggc cca ggc ttt ccc aag gac atg gac ctg gca tgt aaa tac tcc 588
Gly Ala Pro Gly Phe Pro Lys Asp Met Asp Leu Ala Cys Lys Tyr Ser
160 165 170 175

atg aaa gcc tgt gac ctg ggt cat atc tgg gcc tgt gcc aat gcc agt 636

Met Lys Ala Cys Asp Leu Gly His Ile Trp Ala Cys Ala Asn Ala Ser			
176	181	186	191
cgc atg tac aag ctg ggg gat ggt gtt gat aag gat gag gcc aag gcc			684
Arg Met Tyr Lys Leu Gly Asp Gly Val Asp Lys Asp Glu Ala Lys Ala			
192	197	202	207
gag gtg cta aaa aat cga gcc cag cag cta cac aga gaa cag cag aaa			732
Glu Val Leu Lys Asn Arg Ala Gln Gln Leu His Arg Glu Gln Gln Lys			
208	213	218	223
ggt gtc caa ccc tta aca ttt ggg taa tgtgg tccaccctcc ctcccaggca			784
Gly Val Gln Pro Leu Thr Phe Gly *			
224	229		
acaaactgct tgaggctggc agctcctgtt tctgaagact gatgcagccc ttgaaggta			844
acctgctgga gcaaaaaaac ttgggacttg aattttagc tccatttaca tggatccatt			904
gccccagcta ctggagttata gcctacaatg tttatccatg tcaatattcc tttatctggg			964
tgttctgtac aatgtttatt acagtcaata ttccttcatc tggatgttct gtgaagatag			1024
ccatgtttat ggggtctta gtttcaaac tctggcaact ctgtaaaaaa taggagcaaa			1084
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tccagc atg gcc tgg tct cct ctc ctc act ctc ctc gct cac tgc			108
Met Ala Trp Ser Pro Leu Leu Leu Thr Leu Leu Ala His Cys			
1	5	10	
aca ggg tcc tgg gcc cag tct gtg ctg acg cag ccg ccc tca gtg tct			156
Thr Gly Ser Trp Ala Gln Ser Val Leu Thr Gln Pro Pro Ser Val Ser			
15	20	25	30
ggg gcc cca ggg cag agg gtc acc atc tcc tgc act ggg agc agc tcc			204
Gly Ala Pro Gly Gln Arg Val Thr Ile Ser Cys Thr Gly Ser Ser Ser			
31	36	41	46
aac atc ggg gca ggt tat gat gta cac tgg tac cag caa ctt cca gga			252

Asn Ile Gly Ala Gly Tyr Asp Val His Trp Tyr Gln Gln Leu Pro Gly				
47	52	57	62	
aca gcc ccc aaa ctc ctc atc tat ggt aac agc aat cgg ccc tca ggg				300
Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asn Ser Asn Arg Pro Ser Gly				
63	68	73	78	
gtc cct gac cga ttc tct ggc tcc aag tct ggc acc tca gcc tcc ctg				348
Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly Thr Ser Ala Ser Leu				
79	84	89	94	
gcc atc act ggg ctc cag gct gag gat gag gct gat tat tac tgc cag				396
Ala Ile Thr Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Gln				
95	100	105	110	
tcc tat gac agc agc ctg agt ggt tct gtg gta ttc ggc gga ggg acc				444
Ser Tyr Asp Ser Ser Leu Ser Gly Ser Val Val Phe Gly Gly Gly Thr				
111	116	121	126	
aag ctg acc gtc cta ggt cag ccc aag gct gcc ccc tcg gtc act ctg				492
Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu				
127	132	137	142	
ttc ccg ccc ctc ctc tga ggagct tcaagccaac aaggccacac tgggtgtct				546
Phe Pro Pro Leu Leu *				
143	148			
cataagtgac ttctacccgg gagccgtgac agtggcctg				585

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<400> 552

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cgtccggcaa gacctcatct gctgggttac ctcatcctt tagccctct ttgtatgtttg	120
ctgcaaacgt cacccagctc ctggggcaca ctggactccc agatgagtt gtcctggatt	180
tgcaaggagc ctggctccct aaacctttt gccagatccc cacagggaa ttgtgcaggt	240
gcgcctcccc cagatcccc gctggtattt gatatcacacc aactgtcaca catggggagg	300

gcagctgcac ccagccaccc tctgacttct ctcctgccac agattggcca tctgcaagct	360
tcccttctcc gtggagagca ggaagacagt c atg gga cct cag gga gcc agg Met Gly Pro Gln Gly Ala Arg 1 5	412
aga cag gct ttc ttg gca ttt ggg gat gtc act gtg gat ttc acc cag Arg Gln Ala Phe Leu Ala Phe Gly Asp Val Thr Val Asp Phe Thr Gln 8 13 18 23	460
aag gaa tgg agg ctg ctg agc cct gct cag agg gcc ctg tac agg gag Lys Glu Trp Arg Leu Leu Ser Pro Ala Gln Arg Ala Leu Tyr Arg Glu 24 29 34 39	508
gtg aca ctg gag aac tac agc cac ctg gtc tca cta gga att ctc cat Val Thr Leu Glu Asn Tyr Ser His Leu Val Ser Leu Gly Ile Leu His 40 45 50 55	556
tct aaa cca gaa ctc atc agg cgg cta gag caa ggg gaa gtg ccc tgg Ser Lys Pro Glu Leu Ile Arg Arg Leu Glu Gln Gly Glu Val Pro Trp 56 61 66 71	604
gga gaa gag aga aga cgc cgg cca ggc ccc tgt gca gga ata tat gca Gly Glu Glu Arg Arg Pro Gly Pro Cys Ala Gly Ile Tyr Ala 72 77 82 87	652
gaa cat gtc ctg cgg ccc aag aat ctt gga ctt gca cat cag agg caa Glu His Val Leu Arg Pro Lys Asn Leu Gly Leu Ala His Gln Arg Gln 88 93 98 103	700
cag caa cta caa ttt tct gat caa agc ttc cag agt gac aca gct gaa Gln Gln Leu Gln Phe Ser Asp Gln Ser Phe Gln Ser Asp Thr Ala Glu 104 109 114 119	748
ggc caa gag aaa gaa aaa agc act aag ccc atg gca ttt tcc agc cca Gly Gln Glu Lys Glu Lys Ser Thr Lys Pro Met Ala Phe Ser Ser Pro 120 125 130 135	796
ccc cta aga cat gca gta agc tca agg agg agg aac agt gta gtg gaa Pro Leu Arg His Ala Val Ser Ser Arg Arg Asn Ser Val Val Glu 136 141 146 151	844
ata gag tct agt caa ggc cag agg gaa aat cct aca gaa ata gac aaa Ile Glu Ser Ser Gln Gly Gln Arg Glu Asn Pro Thr Glu Ile Asp Lys 152 157 162 167	892
gta ttg aaa gga ata gaa aat tca aga tgg gga gca ttc aag tgt gca Val Leu Lys Gly Ile Glu Asn Ser Arg Trp Gly Ala Phe Lys Cys Ala 168 173 178 183	940
gag cgt ggg caa gac ttc agc cgg aag atg atg gta atc ata cac aaa Glu Arg Gly Gln Asp Phe Ser Arg Lys Met Met Val Ile Ile His Lys 184 189 194 199	988
aaa gca cat tcc agg cag aaa ctt ttt aca tgc agg gag tgt cac cag Lys Ala His Ser Arg Gln Lys Leu Phe Thr Cys Arg Glu Cys His Gln 200 205 210 215	1036

ggc ttt aga gat gag tca gca ttg ctc ttg cac cag aac aca cac aca	216	221	226	231	1084
Gly Phe Arg Asp Glu Ser Ala Leu Leu Leu His Gln Asn Thr His Thr					
gga gag aag tcc tat gtg tgc agt gtg tgt ggg cga ggc ttc agc ctc	232	237	242	247	1132
Gly Glu Lys Ser Tyr Val Cys Ser Val Cys Gly Arg Gly Phe Ser Leu					
aag gcc aac ctc ctc aga cac cag agg aca cac tca gga gag aag cct	248	253	258	263	1180
Lys Ala Asn Leu Leu Arg His Gln Arg Thr His Ser Gly Glu Lys Pro					
ttt ctg tgc aag gtg tgt gga cga ggc tat acc agt aag tca tac ctc	264	269	274	279	1228
Phe Leu Cys Lys Val Cys Gly Arg Gly Tyr Thr Ser Lys Ser Tyr Leu					
act gtg cat gag aga aca cac aca gga gag aag cct tat gaa tgc cag	280	285	290	295	1276
Thr Val His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Gln					
gag tgt ggg cga agg ttt aac gat aag tcc tca tac aac aag cac ttg	296	301	306	311	1324
Glu Cys Gly Arg Arg Phe Asn Asp Lys Ser Ser Tyr Asn Lys His Leu					
aag gcg cat tca ggg gag aag cct ttt gtg tgc aag gag tgt ggg cga	312	317	322	327	1372
Lys Ala His Ser Gly Glu Lys Pro Phe Val Cys Lys Glu Cys Gly Arg					
ggc tat act aat aag tca tac ttc gtt gtg cac aag aga ata cac tca	328	333	338	343	1420
Gly Tyr Thr Asn Lys Ser Tyr Phe Val Val His Lys Arg Ile His Ser					
gga gag aag cct tac aga tgc cag gag tgt ggc cga ggc ttt agc aat	344	349	354	359	1468
Gly Glu Lys Pro Tyr Arg Cys Gln Glu Cys Gly Arg Gly Phe Ser Asn					
aag tca cac ctt atc aca cac cag agg aca cac tca ggg gag aag ccc	360	365	370	375	1516
Lys Ser His Leu Ile Thr His Gln Arg Thr His Ser Gly Glu Lys Pro					
ttt gcg tgc agg cag tgt aag caa agt ttt agc gtg aaa gga agt ctc	376	381	386	391	1564
Phe Ala Cys Arg Gln Cys Lys Gln Ser Phe Ser Val Lys Gly Ser Leu					
ctc aga cac cag aga aca cac tca ggg gag aag cct ttt gtg tgc aag	392	397	402	407	1612
Leu Arg His Gln Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Lys					
gat tgt gag cga agc ttt agc caa aag tca act ctt gtc tac cac cag	408	413	418	423	1660
Asp Cys Glu Arg Ser Phe Ser Gln Lys Ser Thr Leu Val Tyr His Gln					
aga aca cac tca ggg gag aaa cct ttt gtt tgt aga gaa tgt ggg caa	424	429	434	439	1708
Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Arg Glu Cys Gly Gln					

gga ttt att cag aag tca acc ctt gtg aaa cat cag atc aca cac tca Gly Phe Ile Gln Lys Ser Thr Leu Val Lys His Gln Ile Thr His Ser 440 445 450 455	1756
gag gag aag cct ttt gtg tgc aag gac tgt gga cga ggc ttt atc caa Glu Glu Lys Pro Phe Val Cys Lys Asp Cys Gly Arg Gly Phe Ile Gln 456 461 466 471	1804
aag tca acc ttc gct tta cac cag agg aca cac tca gag gag aag cct Lys Ser Thr Phe Ala Leu His Gln Arg Thr His Ser Glu Glu Lys Pro 472 477 482 487	1852
tat gga tgt cgg gag tgt ggg cgt agg ttt cgg gat aag tcc tcc tat Tyr Gly Cys Arg Glu Cys Gly Arg Arg Phe Arg Asp Lys Ser Ser Tyr 488 493 498 503	1900
aac aag cac ctg agg gca cac ttg ggt gag aaa cgt ttt ttc tgc agg Asn Lys His Leu Arg Ala His Leu Gly Glu Lys Arg Phe Phe Cys Arg 504 509 514 519	1948
gat tgt ggg cga ggc ttt acc ttg aag cca aat ctc acc ata cat cag Asp Cys Gly Arg Gly Phe Thr Leu Lys Pro Asn Leu Thr Ile His Gln 520 525 530 535	1996
agg aca cac tca gga gag aag ccc ttc atg tgc aag cag tgt gag aaa Arg Thr His Ser Gly Glu Lys Pro Phe Met Cys Lys Gln Cys Glu Lys 536 541 546 551	2044
agt ttt agt ttg aag gca aat ctt ctt aga cat cag tgg aca cac tcg Ser Phe Ser Leu Lys Ala Asn Leu Arg His Gln Trp Thr His Ser 552 557 562 567	2092
ggg gaa agg cca ttt aat tgc aag gat tgc ggg cga ggc ttc atc cta Gly Glu Arg Pro Phe Asn Cys Lys Asp Cys Gly Arg Gly Phe Ile Leu 568 573 578 583	2140
aaa tca act ctc ctc ttc cac cag aag aca cac tca ggg gag aag cct Lys Ser Thr Leu Leu Phe His Gln Lys Thr His Ser Gly Glu Lys Pro 584 589 594 599	2188
ttc atc tgt agt gaa tgt ggg caa gga ttt atc tgg aag tca aat ctt Phe Ile Cys Ser Glu Cys Gly Gln Gly Phe Ile Trp Lys Ser Asn Leu 600 605 610 615	2236
gtg aaa cac cag ctt gca cat tct ggc aag cag cct ttt gta tgc aag Val Lys His Gln Leu Ala His Ser Gly Lys Gln Pro Phe Val Cys Lys 616 621 626 631	2284
gag tgt ggg cga ggc ttc aac tgg aag gga aat ctc ctc aca cac cag Glu Cys Gly Arg Gly Phe Asn Trp Lys Gly Asn Leu Leu Thr His Gln 632 637 642 647	2332
agg aca cac tca ggg gag aag ccc ttc gtg tgt aat gtg tgt ggg caa Arg Thr His Ser Gly Glu Lys Pro Phe Val Cys Asn Val Cys Gly Gln 648 653 658 663	2380
ggc ttc agc tgg aag aga agt ctc acc aga cac cac tgg cgg ata cac	2428

Gly Phe Ser Trp Lys Arg Ser Leu Thr Arg His His Trp Arg Ile His	664	669	674	679
tca aag gag aag cct ttt gtt tgc cag gag tgt aag cga ggc tat acc				2476
Ser Lys Glu Lys Pro Phe Val Cys Gln Glu Cys Lys Arg Gly Tyr Thr	680	685	690	695
696	701	706	711	
agt aag tca gac ctc act gtg cat gaa aga ata cac aca gga gag agg				2524
Ser Lys Ser Asp Leu Thr Val His Glu Arg Ile His Thr Gly Glu Arg				
712	717	722	727	
cct tat gaa tgc caa gag tgt gga cga aag ttt agc aat aag tca tac				2572
Pro Tyr Glu Cys Gln Glu Cys Gly Arg Lys Phe Ser Asn Lys Ser Tyr				
728	733	738	743	
tac agt aag cac tta aag aga cac tta cgt gag aag cgt ttt tgt aca				2620
Tyr Ser Lys His Leu Lys Arg His Leu Arg Glu Lys Arg Phe Cys Thr				
744	749			
ggg agt gtg ggt gag gct tca tct tga agtta tatctcacca tccatcagag				2672
Gly Ser Val Gly Glu Ala Ser Ser *				
gtttagggtaacc tggcattacc tggcttattt gggaaatgtg gtctttcc tactgagcac				2732
ttcgtgaaga tataacagag gcagacagaa tccagagggc tacagagaac ctgaattcaa				2792
cccatgtgtc cccaagagat tcagagaaaa gaggtcaatg ttttagggAAC agagatgcca				2852
gtttagggtaacc tggcattacc tggcttattt gggaaatgtg gtctttcc tactgagcac				2912
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gcagagcagg gataccaagg caggctgtt acactctccc caacccctt ggactgcaaa				3032
caatcttagga cacctccacc aaaccccttc ttgcactttc cctctggctt ccctcccagc				3092
cttccttggt ttggatgttt tttttttttt ttaattttatg ttgaaactct acataaaactg				3152
tttactgttg aaacagtgtt agtatttagga ggtggaccc ttggaaagtg attaagtcaa				3212
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caaaagatgc agcatgaagg catcatctt gaaacagaca tgagccctca acagacaact				3392
gcacctactg atgttttgc gttgaacttc ccagcctcca gaactctggg aaaataaaagt				3452
cctttata catttccttag tcagtggat tttttttttt cagctcaaat agactaagta				3512
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aaaaaaaaaaaa				3582

<210> 553
 <211> 548
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (268) .. (426)

<400> 553

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tccgaattcg	cggccgcgtc	gacgggggtt	cgattctgct	gactccagtg	gccccagagg	120										
cgccgcttct	tccgcttct	cgtcaggctc	ctgcaacccc	aggcatgaac	caaggtttct	180										
gaactactgg	gcgggagcca	acgtctcttc	tttctccgc	tctggcgag	gctttgtcgc	240										
tgccggctgg	gccccagggt	gtcccccc	atg	gct	ggg	60										
			Met	Ala	Gly	Pro	Arg	Val	Glu	Val	291					
			1			5										
gat	ggc	agc	atc	atg	gaa	ggg	ggc	ggc	cag	atc	ctg	aga	gtc	tct	acg	339
Asp	Gly	Ser	Ile	Met	Glu	Gly	Gly	Gly	Gln	Ile	Leu	Arg	Val	Ser	Thr	
9					14				19					24		
gcc	ttg	agc	tgt	ctc	cta	ggc	ctc	ccc	ttg	cgg	gtg	cag	aag	atc	cga	387
Ala	Leu	Ser	Cys	Leu	Leu	Gly	Leu	Pro	Leu	Arg	Val	Gln	Lys	Ile	Arg	
25					30				35				40			
gcc	ggc	cg	agc	acg	cca	ggc	ctg	agt	att	atg	acc	tga	aggcctcaac	436		
Ala	Gly	Arg	Ser	Thr	Pro	Gly	Leu	Ser	Ile	Met	Thr	*				
41					46				51							
atttatctgg	actggaaatg	attcgagatt	tgtgtatgg	gcaactggag	ggggcagaaa	496										
ttggctcaac	agaaataacc	tttacaccag	agaagatcaa	aggtggaatc	ca	548										

<210> 554
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 <213> Homo sapiens

<220>
 <221> CDS
 <222> (408) .. (2120)

<400> 554

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tcccggggtt	tttcgcgcgc	ggcccccattcc	gcgtgggtga	gtgaatgtga	gagtca	120
tcgcgcgcgc	cgcgcgcgc	gcctccgctg	ttcggcgctc	tgcttttaggc	ggtggggggc	180

gggcgcgcgc	gtaaaagcat	agagacgggc	attgagctct	tgggctagag	cgtcgccgag	240
tcggagccgg	gcctgagcc	gcgcgctgtg	tctccgctgc	gtccgcccag	ccccccgagt	300
gtcagggaca	aaagcctccg	cctgctcccc	cagccggggc	tcatctgccg	ccgcccgcgc	360
gctgaggaga	gttcgcccgc	gtcgccgccc	gtgaggatct	gagagcc	atg tcg gcc	416
					Met Ser Ala	
					1	
agc agc ctc ttg gag cag aga cca aaa ggt caa gga aac aaa gta caa	Ser Ser Leu Leu Glu Gln Arg Pro Lys Gly Gln Gly Asn Lys Val Gln					464
4	9		14		19	
aat gga tct gta cat caa aag gat gga tta aac gat gat gat ttt gaa	Asn Gly Ser Val His Gln Lys Asp Gly Leu Asn Asp Asp Asp Phe Glu					512
20	25		30		35	
cct tac ttg agt cca cag gca agg ccc aat aat gca tat act gcc atg	Pro Tyr Leu Ser Pro Gln Ala Arg Pro Asn Asn Ala Tyr Thr Ala Met					560
36	41		46		51	
tca gat tcc tac tta ccc agt tac tac agt ccc tcc att ggc ttc tcc	Ser Asp Ser Tyr Leu Pro Ser Tyr Tyr Ser Pro Ser Ile Gly Phe Ser					608
52	57		62		67	
tat tct ttg ggt gaa gct gct tgg tct acg ggg ggt gac aca gca gcc atg	Tyr Ser Leu Gly Glu Ala Ala Trp Ser Thr Gly Gly Asp Thr Ala Met					656
68	73		78		83	
ccc tac tta act tct tat gga cag ctg agc aac gga gag ccc cac ttc	Pro Tyr Leu Thr Ser Tyr Gly Gln Leu Ser Asn Gly Glu Pro His Phe					704
84	89		94		99	
cta cca gat gca atg ttt ggg caa cca gga gcc cta ggt agc act cca	Leu Pro Asp Ala Met Phe Gly Gln Pro Gly Ala Leu Gly Ser Thr Pro					752
100	105		110		115	
ttt ctt ggt cag cat ggt ttt aat ttc ttt ccc agt ggg att gac ttc	Phe Leu Gly Gln His Gly Phe Asn Phe Phe Pro Ser Gly Ile Asp Phe					800
116	121		126		131	
tca gca tgg gga aat aac agt tct cag gga cag tct act cag agc tct	Ser Ala Trp Gly Asn Asn Ser Ser Gln Gly Gln Ser Thr Gln Ser Ser					848
132	137		142		147	
gga tat agt agc aat tat gct tat gca cct agc tcc tta ggt gga gcc	Gly Tyr Ser Ser Asn Tyr Ala Tyr Ala Pro Ser Ser Leu Gly Gly Ala					896
148	153		158		163	
atg att gat gga cag tca gct ttt gcc aat gag acc ctc aat aag gct	Met Ile Asp Gly Gln Ser Ala Phe Ala Asn Glu Thr Leu Asn Lys Ala					944
164	169		174		179	
cct ggc atg aat act ata gac caa ggg atg gca gca ctg aag ttg ggt	Pro Gly Met Asn Thr Ile Asp Gln Gly Met Ala Ala Leu Lys Leu Gly					992

180	185	190	195	
agc aca gaa gtt gca agc aat gtt cca aaa gtt gta ggt tct gct gtt				1040
Ser Thr Glu Val Ala Ser Asn Val Pro Lys Val Val Gly Ser Ala Val				
196	201	206	211	
ggt agc ggg tcc att act agt aac atc gtg gct tcc aat agt ttg cct				1088
Gly Ser Gly Ser Ile Thr Ser Asn Ile Val Ala Ser Asn Ser Leu Pro				
212	217	222	227	
cca gcc acc att gct cct cca aaa cca gca tct tgg gct gat att gct				1136
Pro Ala Thr Ile Ala Pro Pro Lys Pro Ala Ser Trp Ala Asp Ile Ala				
228	233	238	243	
agc aag cct gca aaa cag caa cct aaa ctg aag acc aag aat ggc att				1184
Ser Lys Pro Ala Lys Gln Gln Pro Lys Leu Lys Thr Lys Asn Gly Ile				
244	249	254	259	
gca ggg tca agt ctt ccg cca ccc ccg ata aag cat aac atg gat att				1232
Ala Gly Ser Ser Leu Pro Pro Pro Ile Lys His Asn Met Asp Ile				
260	265	270	275	
gga act tgg gat aac aag ggt ccc gtt gca aaa gcc ccc tca cag gct				1280
Gly Thr Trp Asp Asn Lys Gly Pro Val Ala Lys Ala Pro Ser Gln Ala				
276	281	286	291	
ttg gtt cag aat ata ggt cag cca acc cag ggg tct cct cag cct gta				1328
Leu Val Gln Asn Ile Gly Gln Pro Thr Gln Gly Ser Pro Gln Pro Val				
292	297	302	307	
ggt cag cag gct aac aat agc cca cca gtg gct cag gca tca gta ggg				1376
Gly Gln Gln Ala Asn Asn Ser Pro Pro Val Ala Gln Ala Ser Val Gly				
308	313	318	323	
caa cag aca cag cca ttg cct cca cct cca cag cct gcc cag ctt				1424
Gln Gln Thr Gln Pro Leu Pro Pro Pro Gln Pro Ala Gln Leu				
324	329	334	339	
tca gtc cag caa cag gca gct cag cca acc cgc tgg gta gca cct cgg				1472
Ser Val Gln Gln Gln Ala Ala Gln Pro Thr Arg Trp Val Ala Pro Arg				
340	345	350	355	
aac cgt ggc agt ggg ttc ggt cat aat ggg gtg gat ggt aat gga gta				1520
Asn Arg Gly Ser Gly Phe Gly His Asn Gly Val Asp Gly Asn Gly Val				
356	361	366	371	
gga cag tct cag gct ggt tct gga tct act cct tca gaa ccc cac cca				1568
Gly Gln Ser Gln Ala Gly Ser Gly Ser Thr Pro Ser Glu Pro His Pro				
372	377	382	387	
gtg ttg gag aag ctt cgg tcc att aat aac tat aac ccc aaa gat ttt				1616
Val Leu Glu Lys Leu Arg Ser Ile Asn Asn Tyr Asn Pro Lys Asp Phe				
388	393	398	403	
gac tgg aat ctg aaa cat ggc cgg gtt ttc atc att aag agc tac tct				1664
Asp Trp Asn Leu Lys His Gly Arg Val Phe Ile Ile Lys Ser Tyr Ser				
404	409	414	419	

gag gac gat att cac cgt tcc att aag tat aat att tgg tgc agc aca Glu Asp Asp Ile His Arg Ser Ile Lys Tyr Asn Ile Trp Cys Ser Thr 420 425 430 435	1712
gag cat ggt aac aag aga ctg gat gct gct tat cgt tcc atg aac ggg Glu His Gly Asn Lys Arg Leu Asp Ala Ala Tyr Arg Ser Met Asn Gly 436 441 446 451	1760
aaa ggc ccc gtt tac tta ctt ttc agt gtc aac ggc agt gga cac ttc Lys Gly Pro Val Tyr Leu Leu Phe Ser Val Asn Gly Ser Gly His Phe 452 457 462 467	1808
tgt ggc gtg gca gaa atg aaa tct gct gtg gac tac aac aca tgt gca Cys Gly Val Ala Glu Met Lys Ser Ala Val Asp Tyr Asn Thr Cys Ala 468 473 478 483	1856
ggg gtg tgg tcc cag gac aaa tgg aag ggt cgt ttt gat gtc agg tgg Gly Val Trp Ser Gln Asp Lys Trp Lys Gly Arg Phe Asp Val Arg Trp 484 489 494 499	1904
att ttt gtg aag gac gtt ccc aat agc caa ctg cga cac att cgc cta Ile Phe Val Lys Asp Val Pro Asn Ser Gln Leu Arg His Ile Arg Leu 500 505 510 515	1952
gag aac aac gag aat aaa cca gtg acc aac tct agg gac act cag gaa Glu Asn Asn Glu Asn Lys Pro Val Thr Asn Ser Arg Asp Thr Gln Glu 516 521 526 531	2000
gtg cct ctg gaa aag gct aag cag gtg ttg aaa att ata gcc agc tac Val Pro Leu Glu Lys Ala Lys Gln Val Leu Lys Ile Ile Ala Ser Tyr 532 537 542 547	2048
aag cac acc act tcc att ttt gat gac ttc tca cac tat gag aaa cgc Lys His Thr Thr Ser Ile Phe Asp Asp Phe Ser His Tyr Glu Lys Arg 548 553 558 563	2096
cca aga gga aga aga aag tgt taa aaaggaacgt caaggtcggt gggaaaaaaa Pro Arg Gly Arg Arg Lys Cys *	2150
564 569	
ggcagttcta cacagactgc agcaacgggt gcacatctgcat atcctaagag gaaaaaatga	2210
ccttcaagag aattaggact tttttcttaa tttcactgac ttcagagacg attgcagact	2270
tgcagttaa gtatttggaaat ttcacaaaag acataggact taactggaaa atgaaaaaaaa	2330
aaagaaaaag aaaaaactaa ccaaaaaatc cctctaggta gtttagggaa aaaatgtccc	2390
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ttcctcctcc cattttgaca tttgcacttg gagaacactt gagttgtgaa gggtttggc	2570
atccacccca gaaagtggga atttgattt atccttccga actggaaagaa cattttatg	2630

aagaatttt	gtctaggaga	atataaacagt	gttacccaag	gttgtgtctt	taagggtggt	2690
tcattttctc	tgacctttg	ttactcaaag	taaagtacta	ggagtcctaa	gaaatgttct	2750
gttcttgtac	attataactga	ttaagtcaagg	attaatttga	tttcaaagct	gagaacagtg	2810
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gactcctagt	actttacttt	gagtaacaaa	aggtcagaga	aatgaacca	cccttaaaga	2990
cacaaccttg	ggtaacactg	ttatattctc	ctagacaaaa	attcttcata	aaaatgttct	3050
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cagttaagtc	ctatgtctt	tgtgaaattc	caatacttaa	actgcaagtc	tgcaatcg	3410
tctgaagtca	gtgaaattaa	gaaaaaaagtc	ctaattctct	tgaaggtcat	ttttccctct	3470
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acttgacgt	tcctacagag	gtaagaaaaa	aattgaaatg	gttaaaaatt	atctgaacat	3590
gccttatgaa	tttaaaaact	tcacagaata	actcaacaga	aatttaatta	tttagaatta	3650
ttagaaaatt	aattatttta	agtagaaacat	tccccacaaa	gaaaaactgg	cttttacttt	3710
gttttaaaca	cttaaacacc	ttaatgcaaa	attactttg	acttgaaaat	tcattacatg	3770
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<210> 555
 <211> 4352
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (77) .. (1978)

<400> 555
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60

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	Met Glu Leu Ala Gln Glu Ala Arg Glu Leu Gly			
12	17	22	27	157
gaa tcg acg ctg cgc agg ctg tgt ctg ggc cag ggg gct gac atc tgg				205
Glu Ser Thr Leu Arg Arg Leu Cys Leu Gly Gln Gly Ala Asp Ile Trp				
28	33	38	43	
gcc tac atc ttg cag cat gtg cac agt cag agg act gtc aag aag atc				253
Ala Tyr Ile Leu Gln His Val His Ser Gln Arg Thr Val Lys Lys Ile				
44	49	54	59	
cgg gga aac cta ctc tgg tat ggc cac cag gac agt cca cag gtc cgt				301
Arg Gly Asn Leu Leu Trp Tyr Gly His Gln Asp Ser Pro Gln Val Arg				
60	65	70	75	
cgg aag tta gag ctg gaa gct gct gtg acc cgc ctg cgg gca gaa atc				349
Arg Lys Leu Glu Leu Glu Ala Ala Val Thr Arg Leu Arg Ala Glu Ile				
76	81	86	91	
cag gaa ctc gac cag agc ctg gag ctg atg gag cga gac act gag gct				397
Gln Glu Leu Asp Gln Ser Leu Glu Leu Met Glu Arg Asp Thr Glu Ala				
92	97	102	107	
cag gac acg gcc atg gag cag gca cgt cag cac act caa gac acc cag				445
Gln Asp Thr Ala Met Glu Gln Ala Arg Gln His Thr Gln Asp Thr Gln				
108	113	118	123	
cgt cga gct ctc ctc cgg gcc caa gct ggg gcc atg cga aga cag				493
Arg Arg Ala Leu Leu Leu Arg Ala Gln Ala Gly Ala Met Arg Arg Gln				
124	129	134	139	
cag cat acg ctc cga gat ccc atg cag cgg ctg cag aat caa ctg agg				541
Gln His Thr Leu Arg Asp Pro Met Gln Arg Leu Gln Asn Gln Leu Arg				
140	145	150	155	
cgc ctg cag gac atg gag agg aaa gcc aaa gta gat gtg acc ttt gga				589
Arg Leu Gln Asp Met Glu Arg Lys Ala Lys Val Asp Val Thr Phe Gly				
156	161	166	171	
tcc ctc acg tcg gca gct ctg ggc ctg gag ccc gtg gtc ctg cgt gat				637
Ser Leu Thr Ser Ala Ala Leu Gly Leu Glu Pro Val Val Leu Arg Asp				
172	177	182	187	
gtc cga aca gcc tgc acc ctc cgg gcc cag ttc ctg cag aac ctc ctg				685
Val Arg Thr Ala Cys Thr Leu Arg Ala Gln Phe Leu Gln Asn Leu Leu				
188	193	198	203	
ctt ccc cag gcc aag agg ggc agc ctc cca acc cct cat gat gac cac				733
Leu Pro Gln Ala Lys Arg Gly Ser Leu Pro Thr Pro His Asp Asp His				
204	209	214	219	
ttt ggc act tcg tac cag cag tgg ctg agc tca gtg gag acg ctg ctg				781

Phe	Gly	Thr	Ser	Tyr	Gln	Gln	Trp	Leu	Ser	Ser	Val	Glu	Thr	Leu	Leu	
220					225			230				235				
aca	aac	cac	ccc	cca	ggc	cac	gtc	ctg	gtc	gcc	ttg	gag	cac	ctg	gct	829
Thr	Asn	His	Pro	Pro	Gly	His	Val	Leu	Ala	Ala	Leu	Glu	His	Leu	Ala	
236					241			246				251				
gca	gag	cg	gag	gca	gag	gtt	cg	g	tc	tc	tg	tc	ag	g	gg	877
Ala	Glu	Arg	Glu	Ala	Glu	Val	Arg	Ser	Leu	Cys	Ser	Gly	Asp	Gly	Leu	
252				257			262			267						
ggc	gac	aca	gag	ata	tcc	aga	ccc	cag	ggc	ccg	gac	cag	tca	gac	tcc	925
Gly	Asp	Thr	Glu	Ile	Ser	Arg	Pro	Gln	Ala	Pro	Asp	Gln	Ser	Asp	Ser	
268				273			278			283						
agc	cag	acc	ctg	ccg	tcc	atg	gtt	cat	ctc	atc	cag	gag	ggc	tgg	cg	973
Ser	Gln	Thr	Leu	Pro	Ser	Met	Val	His	Leu	Ile	Gln	Glu	Gly	Trp	Arg	
284				289			294			299						
act	gtg	ggt	gtg	ctg	gtc	tcc	cag	cg	agc	acc	ctc	ctg	aag	gag	cg	1021
Thr	Val	Gly	Val	Leu	Val	Ser	Gln	Arg	Ser	Thr	Leu	Leu	Lys	Glu	Arg	
300				305			310			315						
caa	gtc	ttg	acc	cag	cg	ctc	cag	ggc	ctg	gtg	gag	gtg	gag	aga		1069
Gln	Val	Leu	Thr	Gln	Arg	Leu	Gln	Gly	Leu	Val	Glu	Glu	Val	Glu	Arg	
316				321			326			331						
cg	gc	ctg	gga	tcc	agt	gag	agg	cag	gt	ctg	ata	ctg	gg	ctt	cg	1117
Arg	Val	Leu	Gly	Ser	Ser	Glu	Arg	Gln	Val	Leu	Ile	Leu	Gly	Leu	Arg	
332				337			342			347						
cg	cg	tgt	tgc	ctg	tgg	ac	gag	ctc	aag	ggc	ctg	cac	gat	cag	ac	1165
Arg	Cys	Cys	Leu	Trp	Thr	Glu	Leu	Lys	Ala	Leu	His	Asp	Gln	Ser	Gln	
348				353			358			363						
gag	ctg	cag	gat	gca	gct	gg	cat	cg	cg	ctc	ctg	ctg	agg	gag	ct	1213
Glu	Leu	Gln	Asp	Ala	Ala	Gly	His	Arg	Gln	Leu	Leu	Leu	Arg	Glu	Leu	
364				369			374			379						
cag	gc	aaa	cag	cag	cg	atc	ctg	cac	tgg	cg	cag	ctg	gtg	gag	gag	1261
Gln	Ala	Lys	Gln	Gln	Arg	Ile	Leu	His	Trp	Arg	Gln	Leu	Val	Glu	Glu	
380				385			390			395						
acc	cag	gaa	cag	cag	gtc	cg	ctg	ctc	atc	aag	gg	aac	tc	gc	ag	1309
Thr	Gln	Gln	Val	Arg	Leu	Leu	Ile	Lys	Gly	Asn	Ser	Ala	Ser	Lys		
396				401			406			411						
acc	cg	ctg	tgc	cg	ag	cc	gg	gag	gt	ct	ct	gt	cag	cg		1357
Thr	Arg	Leu	Cys	Arg	Ser	Pro	Gly	Glu	Val	Leu	Ala	Leu	Val	Gln	Arg	
412				417			422			427						
aag	gt	gt	cct	aca	ttt	gag	gca	gt	gca	cc	cag	ag	cg	gag	ct	1405
Lys	Val	Val	Pro	Thr	Phe	Glu	Ala	Val	Ala	Pro	Gln	Ser	Arg	Glu	Leu	
428				433			438			443						
ctg	cg	tgt	ctg	gag	gag	gaa	gtc	cg	cat	ttg	cc	cac	att	ctg	tt	1453
Leu	Arg	Cys	Leu	Glu	Glu	Val	Arg	His	Leu	Pro	His	Ile	Leu	Leu		

444	449	454	459	
ggc acg ctg ctg cg	cac agg ccg gga gag ttg aag ccc ctg ccc acg			1501
Gly Thr Leu Leu Arg	His Arg Pro Gly Glu Leu Lys Pro Leu Pro Thr			
460	465	470	475	
gtc ctc cca tcc atc cac cag ctg cac ccc g	cg tcc cca agg ggc tcc			1549
Val Leu Pro Ser Ile His Gln Leu His Pro Ala Ser Pro Arg Gly Ser				
476	481	486	491	
agc ttc ata gcg ctg agc cac aag ctg ggg ctg cct cca ggg aag gcc				1597
Ser Phe Ile Ala Leu Ser His Lys Leu Gly Leu Pro Pro Gly Lys Ala				
492	497	502	507	
tcg gag ctg ctc ctg ccg gcg gct gcc tct ctt cgc cag gac ctt ctg				1645
Ser Glu Leu Leu Leu Pro Ala Ala Ser Leu Arg Gln Asp Leu Leu				
508	513	518	523	
ctc ctg cag gac cag cgg agc ctc tgg tgc tgg gat cta ctc cac atg				1693
Leu Leu Gln Asp Gln Arg Ser Leu Trp Cys Trp Asp Leu Leu His Met				
524	529	534	539	
aag acc agc ctg ccg cca ggc ctt ccc acc cag gag ctg ctg cag atc				1741
Lys Thr Ser Leu Pro Pro Gly Leu Pro Thr Gln Glu Leu Leu Gln Ile				
540	545	550	555	
cag gca tcc cag gaa aaa cag cag aaa gag aac ctg ggg cag gct ctg				1789
Gln Ala Ser Gln Glu Lys Gln Gln Lys Glu Asn Leu Gly Gln Ala Leu				
556	561	566	571	
aag agg ctg gag aag cta ctg aaa cag gca ctg gag cga atc cct gag				1837
Lys Arg Leu Glu Lys Leu Leu Lys Gln Ala Leu Glu Arg Ile Pro Glu				
572	577	582	587	
ctg cag ggg atc gtg ggg gac tgg tgg gag cag cca ggc cag gcc g				1885
Leu Gln Gly Ile Val Gly Asp Trp Trp Glu Gln Pro Gly Gln Ala Ala				
588	593	598	603	
ctc tct gag gag ctc tgc cag ggc ctg tcc ctg ccc cag tgg cgg ctg				1933
Leu Ser Glu Glu Leu Cys Gln Gly Leu Ser Leu Pro Gln Trp Arg Leu				
604	609	614	619	
cgc tgg gtt cag gcc cag ggg gcc ctg cag aag ctg tgc agc tga aga				1981
Arg Trp Val Gln Ala Gln Gly Ala Leu Gln Lys Leu Cys Ser *				
620	625	630		
gagggttcaa acggaagccg agaacttgac actgttccacc ccaacacccctc acctccccca				2041
ggacatttgg aagaaagcag cgccaggatt cctcggcagt cgtccccacc cgcacctgca				2101
gtccccctcat gtgctgttct gctgccccac tcagctcctg gaccctgtcc tttcatcccg				2161
ctaaagcacc ccctaaaacc cttcatcac ttcatctc agaaaaagt aattgagcac				2221
ctcctctagg cgctggggag tccacactga aaaaaagaaa cagaaaaaccc tgtcttccag				2281
cagttgagtt ctagggcagg gagacagagt ttacaagata aggaaaatat atatgttagta				2341

tgctgcaagt taactgctgt gtggaaatc cagcaggggg tggatgtgt gatttgaatt 2401
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gctggcccca gaagaaaaac atgcacagat ggtatgttca ctgggtgtgc agtaagttt 3841
caaatttggaa agtttggcag ctttatgatc ttgaaccttg ctgtccatct ctcacacaac 3901
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gtttccctggc ctttccacat tggctttccc atgtatgcct tagtgtgtct gtcctccctc 4021

tctctcctca tcacagttcc cagcccccac cttcaactga actcaacaaa atcttcaact	4081
tcatacagta gtcacattgt tagtaataac actggcattt ttatttgat aaaatagacc	4141
gtttaaattt ttgagattct accttatatt tttgaatta tataactaaag caaataagta	4201
gtgatgtaat gtcattgggg accaagattt ttagtgtaaa tgaaaaaaga taacaaatat	4261
aaactcaagt aaacaccctg tagtcttca catgaattgg aaatatcaga ataaagtcat	4321
gattttctc tttctaaaaa aaaaaaaaaa a	4352

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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (188)..(1108)

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ctgggctgga ccgaaaccgg cgccggagcaa ctgaggcccg agccttctcg ggacccgggg	120
gacgcctaac cccgcgagaa ccctgcaaattttcttcctc ataattggaa gaagactcac	180
tggccga atg gca gca gta gat gac ttg caa ttt gaa gaa ttt ggc aat	229
Met Ala Ala Val Asp Asp Leu Gln Phe Glu Glu Phe Gly Asn	
1 5 10	
gca gcc act tct ctg aca gca aac cca gat gcc acc aca gta aac att	277
Ala Ala Thr Ser Leu Thr Ala Asn Pro Asp Ala Thr Thr Val Asn Ile	
15 20 25 30	
gag gat cct ggt gaa acc cca aaa cat cag cca gga tcc cca aga ggc	325
Glu Asp Pro Gly Glu Thr Pro Lys His Gln Pro Gly Ser Pro Arg Gly	
31 36 41 46	
tca gga aga gaa gaa gat gat gag tta ctg gga aat gat gac tct gac	373
Ser Gly Arg Glu Asp Asp Glu Leu Leu Gly Asn Asp Asp Ser Asp	
47 52 57 62	
aaa act gag tta ctt gct gga cag aag aaa agc tcc ccc ttc tgg aca	421
Lys Thr Glu Leu Leu Ala Gly Gln Lys Ser Ser Pro Phe Trp Thr	
63 68 73 78	
ttt gaa tac tac caa aca ttc ttt gat gtg gac acc tac cag gtc ttt	469
Phe Glu Tyr Tyr Gln Thr Phe Phe Asp Val Asp Thr Tyr Gln Val Phe	
79 84 89 94	
gac aga att aaa gga tct ctt ttg cca ata ccc ggg aaa aac ttt gtg	517
Asp Arg Ile Lys Gly Ser Leu Leu Pro Ile Pro Gly Lys Asn Phe Val	

95	100	105	110	
agg tta tat atc cgc agc aat cca gat ctc tat ggc ccc ttt tgg ata				565
Arg Leu Tyr Ile Arg Ser Asn Pro Asp Leu Tyr Gly Pro Phe Trp Ile				
111	116	121	126	
tgt gcc acg ttg gtc ttt gcc ata gca att agt ggg aat ctt tcc aac				613
Cys Ala Thr Leu Val Phe Ala Ile Ala Ser Gly Asn Leu Ser Asn				
127	132	137	142	
ttc ttg atc cat ctg gga gag aag acg tac cat tat gtg ccc gaa ttc				661
Phe Leu Ile His Leu Gly Glu Lys Thr Tyr His Tyr Val Pro Glu Phe				
143	148	153	158	
cga aaa gtg tcc ata gca gct acc atc atc tat gcc tat gcc tgg ctg				709
Arg Lys Val Ser Ile Ala Ala Thr Ile Ile Tyr Ala Tyr Ala Trp Leu				
159	164	169	174	
gtt cct ctt gca ctc tgg ggt ttc ctc atg tgg aga aac acg aaa gtt				757
Val Pro Leu Ala Leu Trp Gly Phe Leu Met Trp Arg Asn Ser Lys Val				
175	180	185	190	
atg aac atc gtc tcc tat tca ttt ctg gag att gtg tgt gtc tat gga				805
Met Asn Ile Val Ser Tyr Ser Phe Leu Glu Ile Val Cys Val Tyr Gly				
191	196	201	206	
tat tcc ctc ttc att tat atc ccc acc gca ata ctg tgg att atc ccc				853
Tyr Ser Leu Phe Ile Tyr Ile Pro Thr Ala Ile Leu Trp Ile Ile Pro				
207	212	217	222	
cag aaa gct gtt cgt tgg att cta gtc atg att gcc ctg ggc atc tca				901
Gln Lys Ala Val Arg Trp Ile Leu Val Met Ile Ala Leu Gly Ile Ser				
223	228	233	238	
gga tct ctc ttg gca atg aca ttt tgg cca gct gtt cgt gag gat aac				949
Gly Ser Leu Leu Ala Met Thr Phe Trp Pro Ala Val Arg Glu Asp Asn				
239	244	249	254	
cga cgc gtt gca ttg gcc aca att gtg aca att gtg ttg ctc cat atg				997
Arg Arg Val Ala Leu Ala Thr Ile Val Thr Ile Val Leu Leu His Met				
255	260	265	270	
ctg ctt tct gtg ggc tgc ttg gca tac ttt ttt gat gca cca gag atg				1045
Leu Leu Ser Val Gly Cys Leu Ala Tyr Phe Phe Asp Ala Pro Glu Met				
271	276	281	286	
gac cat ctc cca aca act aca gct act cca aac caa aca gtt gct gca				1093
Asp His Leu Pro Thr Thr Ala Thr Pro Asn Gln Thr Val Ala Ala				
287	292	297	302	
gcc aag tcc agc taa tgaggaaaga ctcacttgag ataccctctc cttgctgaag				1148
Ala Lys Ser Ser *				
303				
tttttcttga cttctccagt tctctttgt tttttggagc atgggttcttt ggaaagtggc				1208
atccactgca ggaaagcaga atgagcagag ccagcagaac tcatggagtg gcacaaattc				1268

ccagtgtctg gatggtgcca cactggcgcc taatcacccg tttaacaagc agaaattaaa	1328
tgttgctcag cacatgtgtc tttcagctct tcctttcac ccatggatga tcattgcgag	1388
catgcgctga ttggactgaa atgccgggaa ataggtagg catgctcagt gccgtccctt	1448
tgccaccaca gtcaaattgac atgcttcaact gtggtacctt aatacctgaa atagaaccat	1508
ggaaaattct gatgtcctct ctctgaattt tgtacagact acctggggaa tcctcttctc	1568
tccaaatgtt agccatcctg aagtagccga acagtagaaa ctttgggtgg gattaaccgg	1628
gagcttgaaa atttgtctt ggttaacctga tactggacag ctgtactgaa tggctgcaaa	1688
ataaatacct cacatgatgt ctgtgtctgc aaaaaaaaaaaa aaa	1731

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (259)..(1377)

<400> 557

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ccgccattga cacgcacaga tagaacccaa agaaaggcaa agagtcctgc ccggcaccgg	120
cgcgcgtgg gccaaacctg cgcccggtga gggggcgcgca gagggcaccgg ggcgcgggaa	180
gcaggcggcg cagcaccagc attgtgttag tgccgggagg ccactgtgtc agcaagctga	240
gagggaaact gaagcaag atg tcg ggc cgg agt ggg aag aag aaa atg tcc	291
Met Ser Gly Arg Ser Gly Lys Lys Lys Met Ser	
1 5	

aag ctg tcc cgt tca gct agg gca ggt gtc atc ttt cca gtg ggg agg	339
Lys Leu Ser Arg Ser Ala Arg Ala Gly Val Ile Phe Pro Val Gly Arg	
12 17 22 27	

ctg atg cgt tat ctg aag aaa ggg acg ttc aag tac cgg atc agc gtg	387
Leu Met Arg Tyr Leu Lys Lys Gly Thr Phe Lys Tyr Arg Ile Ser Val	
28 33 38 43	

ggc gcc cct gtc tac atg gcg gca gtc att gag tac ctg gca gcg gaa	435
Gly Ala Pro Val Tyr Met Ala Ala Val Ile Glu Tyr Leu Ala Ala Glu	
44 49 54 59	

att cta gaa ttg gcc ggc aat gcc gcg agg gac aac aag aag gcc cgg	483
Ile Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys Ala Arg	
60 65 70 75	

ata gcc ccg aga cac atc ttg ctg gca gtt gcc aat gac gag gag ctc Ile Ala Pro Arg His Ile Leu Leu Ala Val Ala Asn Asp Glu Glu Leu 76 81 86 91	531
aac cag ctg cta aaa gga gtg acc atc gcc agt gga ggc gtc ctg ccc Asn Gln Leu Leu Lys Gly Val Thr Ile Ala Ser Gly Gly Val Leu Pro 92 97 102 107	579
aga att cac ccc gaa ctg ctg gcc aaa aag cga ggg acc aaa ggc aag Arg Ile His Pro Glu Leu Leu Ala Lys Lys Arg Gly Thr Lys Gly Lys 108 113 118 123	627
tcg gaa acg atc ctc tcc cca ccc cca gag aaa aga ggc agg aag gcc Ser Glu Thr Ile Leu Ser Pro Pro Pro Glu Lys Arg Gly Arg Lys Ala 124 129 134 139	675
acg tca ggc aag aag ggg ggg aag aaa tcc aag gct gcc aaa cca cgg Thr Ser Gly Lys Lys Gly Lys Ser Lys Ala Ala Lys Pro Arg 140 145 150 155	723
acg tcc aaa aag tcc aaa cca aag gac agc gat aaa gaa gga act tca Thr Ser Lys Lys Ser Lys Pro Lys Asp Ser Asp Lys Glu Gly Thr Ser 156 161 166 171	771
aat tcc acc tct gaa gat ggg cca ggg gat gga ttc acc att ctg tct Asn Ser Thr Ser Glu Asp Gly Pro Gly Asp Gly Phe Thr Ile Leu Ser 172 177 182 187	819
tct aag agc ctt gtt ctg gga cag aag ctg tcc tta acc cag agt gac Ser Lys Ser Leu Val Leu Gly Gln Lys Leu Ser Leu Thr Gln Ser Asp 188 193 198 203	867
atc agc cat att ggc tcc atg aga gtg gag ggc att gtc cac cca acc Ile Ser His Ile Gly Ser Met Arg Val Glu Gly Ile Val His Pro Thr 204 209 214 219	915
aca gcc gaa att gac ctc aaa gaa gat ata ggt aaa gcc ttg gaa aag Thr Ala Glu Ile Asp Leu Lys Glu Asp Ile Gly Lys Ala Leu Glu Lys 220 225 230 235	963
gct ggg gga aaa gag ttc ttg gaa acg gta aag gag ctt cgc aaa tcc Ala Gly Gly Lys Glu Phe Leu Glu Thr Val Lys Glu Leu Arg Lys Ser 236 241 246 251	1011
caa ggc cct ttg gaa gtc gcc gaa gcc gcc gtc agc caa tcc agt gga Gln Gly Pro Leu Glu Val Ala Glu Ala Ala Val Ser Gln Ser Ser Gly 252 257 262 267	1059
ctc gca gcc aaa ttt gtc atc cac tgt cac atc cct cag tgg ggc tcc Leu Ala Ala Lys Phe Val Ile His Cys His Ile Pro Gln Trp Gly Ser 268 273 278 283	1107
gac aaa tgt gaa gaa cag ctt gaa gag acc atc aaa aac tgc ctg tca Asp Lys Cys Glu Glu Gln Leu Glu Glu Thr Ile Lys Asn Cys Leu Ser 284 289 294 299	1155

gcg gcg gag gac aag aag cta aag tcc gtc gcg ttc ccg cct ttc ccc Ala Ala Glu Asp Lys Lys Leu Lys Ser Val Ala Phe Pro Pro Phe Pro 300 305 310 315	1203
agc ggc aga aac tgc ttt ccc aaa cag act gcg gcc cag gtg acc ctc Ser Gly Arg Asn Cys Phe Pro Lys Gln Thr Ala Ala Gln Val Thr Leu 316 321 326 331	1251
aaa gcc atc tca gcc cac ttt gat gac tcg agc gcg tcc tcg ctg aag Lys Ala Ile Ser Ala His Phe Asp Asp Ser Ser Ala Ser Ser Leu Lys 332 337 342 347	1299
aac gtg tac ttc ctg ctc ttc gac agc gag agc atc ggc atc tac gtg Asn Val Tyr Phe Leu Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr Val 348 353 358 363	1347
cag gag atg gcc aag ctc gac gcc aag tag c cgccgcactt tccagcaggg Gln Glu Met Ala Lys Leu Asp Ala Lys *	1398
364 369	
atcggaggac gacccgagtc ccaagagtgg ggtttgctt tttaaaagga gagaggaggg	1458
gtgatggcag gggagtgag gggtggccggg caggtcctgc cggcgcaggg agccctctgc	1518
ccttcacact ctcctccaaa agagcctcca tctgtaagga agcaggtctc cgcgaggggt	1578
ttctttccat gtgtttcct cctgttggtt tagaactttt ttaaaaaaac agacctcggtt	1638
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cttaaaaaaaa aaaaaaaaa	1716

<210> 558
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (187)..(846)

<400> 558 atttggccct cgaggccaag aattcggcac gaggactaac acacctctaa catttcaccc ctagctcaga tgagagagag aatgggactt cttggtactg attgttttc ccatgcctca atggtttct ttttagggagc tacaaattta cgggttcaact ggtgattgat ctttcatcc agcaca atg gac aga agt cta agg aac gtc ctt gtg gtt tcc ttt ggg Met Asp Arg Ser Leu Arg Asn Val Leu Val Val Ser Phe Gly 1 5 10	60
ttc ctg ctt ctc ttt aca gcc tat gga ggt ctg cag agc ctg cag agc Phe Leu Leu Leu Phe Thr Ala Tyr Gly Gly Leu Gln Ser Leu Gln Ser	276

15	20	25	30	
agc ctg tac agc gag gag ggc ctg ggt gtc aca gcg ctc agc acc ctc				324
Ser Leu Tyr Ser Glu Glu Gly Leu Gly Val Thr Ala Leu Ser Thr Leu				
31	36	41	46	
tat gga ggc atg ctc ctg tcc atg ttc ctc cca ccg ctc ctc atc				372
Tyr Gly Gly Met Leu Leu Ser Ser Met Phe Leu Pro Pro Leu Leu Ile				
47	52	57	62	
gag agg ctg ggc tgc aag ggg acc atc atc ctc tcc atg tgt ggc tac				420
Glu Arg Leu Gly Cys Lys Gly Thr Ile Ile Leu Ser Met Cys Gly Tyr				
63	68	73	78	
gtg gcc ttc tcc gtg ggc aac ttc ttc gcc agc tgg tac act ttg atc				468
Val Ala Phe Ser Val Gly Asn Phe Ala Ser Trp Tyr Thr Leu Ile				
79	84	89	94	
ccc acc tcc ata ctg ctg gga ctc ggg gcc gcc ccg ctg tgg tct gca				516
Pro Thr Ser Ile Leu Leu Gly Leu Gly Ala Ala Pro Leu Trp Ser Ala				
95	100	105	110	
cag tgc aca tac ctc acg atc acg gga aac aca cat gca gag aag gcg				564
Gln Cys Thr Tyr Leu Thr Ile Thr Gly Asn Thr His Ala Glu Lys Ala				
111	116	121	126	
gga aag cgt ggc aaa gac atg gtg aac cag tat ttt ggc atc ttc ttc				612
Gly Lys Arg Gly Lys Asp Met Val Asn Gln Tyr Phe Gly Ile Phe Phe				
127	132	137	142	
ctc ata ttc cag tca tcc ggt gtg tgg ggc aac ttg atc tca tcg ctg				660
Leu Ile Phe Gln Ser Ser Gly Val Trp Gly Asn Leu Ile Ser Ser Leu				
143	148	153	158	
gta ttt ggc cag act ccc agc caa gag acc ctt cca gaa gag cag ctc				708
Val Phe Gly Gln Thr Pro Ser Gln Glu Thr Leu Pro Glu Glu Gln Leu				
159	164	169	174	
acg tcc tgt ggg gcc agt gac tgc ctg atg gcc acc aca acc acc aac				756
Thr Ser Cys Gly Ala Ser Asp Cys Leu Met Ala Thr Thr Thr Asn				
175	180	185	190	
agc acc cag agg ccc tcc cag cag ctg gtc tac acc ctc ctg ggc atc				804
Ser Thr Gln Arg Pro Ser Gln Gln Leu Val Tyr Thr Leu Leu Gly Ile				
191	196	201	206	
tac act ggt acg agc tcc atc ggc cca ggg cag ggt ccc tag caaagca				853
Tyr Thr Gly Thr Ser Ser Ile Gly Pro Gly Gln Gly Pro *				
207	212	217		
gagccaagcc tccttcctgg gctgacaaaag actgtctctc ccaatgtaaa aagtaatctc				913
tcttc				918

<210> 559
<211> 2511
<212> DNA
<213> Homo sapiens

<220>
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<222> (47) .. (2233)

<400> 559

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	Met Ala Gly	
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ttc tgg gtc ggg aca gca ccg ctg gtc gct gcc gga cgg cgt ggg cgg		103
Phe Trp Val Gly Thr Ala Pro Leu Val Ala Ala Gly Arg Arg Gly Arg		
4 9 14 19		
tgg ccg ccg cag cag ctg atg ctg agc gcg gcg ctg cgg acc ctg aag		151
Trp Pro Pro Gln Gln Leu Met Leu Ser Ala Ala Leu Arg Thr Leu Lys		
20 25 30 35		
cat gtt ctg tac tat tca aga cag tgc tta atg gtg tcc cgt aat ctt		199
His Val Leu Tyr Tyr Ser Arg Gln Cys Leu Met Val Ser Arg Asn Leu		
36 41 46 51		
ggt tca gtg gga tat gat cct aat gaa aaa act ttt gat aaa att ctt		247
Gly Ser Val Gly Tyr Asp Pro Asn Glu Lys Thr Phe Asp Lys Ile Leu		
52 57 62 67		
gtt gct aat aga gga gaa att gca tgt cgg gtt att aga act tgc aag		295
Val Ala Asn Arg Gly Glu Ile Ala Cys Arg Val Ile Arg Thr Cys Lys		
68 73 78 83		
aag atg ggc att aag aca gtt gcc atc cac agt gat gtt gat gct agt		343
Lys Met Gly Ile Lys Thr Val Ala Ile His Ser Asp Val Asp Ala Ser		
84 89 94 99		
tct gtt cat gtg aaa atg gcg gat gag gct gtc tgt gtt ggc cca gct		391
Ser Val His Val Lys Met Ala Asp Glu Ala Val Cys Val Gly Pro Ala		
100 105 110 115		
ccc acc agt aaa agc tac ctc aac atg gat gcc atc atg gaa gcc att		439
Pro Thr Ser Lys Ser Tyr Leu Asn Met Asp Ala Ile Met Glu Ala Ile		
116 121 126 131		
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Lys Lys Thr Arg Ala Gln Ala Val His Pro Gly Tyr Gly Phe Leu Ser		
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Ile Gly Pro Asp Thr His Ala Ile Gln Ala Met Gly Asp Lys Ile Glu		
164 169 174 179		

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agg act gtc cag tgt ctt tct cga gaa gca ggt gga aac atg agc att Arg Thr Val Gln Cys Leu Ser Arg Glu Ala Gly Gly Asn Met Ser Ile 612 617 622 627	1927
cag ttt ctt ggt aca gtg tac aag gtg aat atc tta acc aga ctt gcc	1975

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Ala Glu Leu Asn Lys Phe Met Leu Glu Lys Val Thr Glu Asp Thr Ser				
644	649	654	659	
agt gtt ctg cgt tcc ccg atg ccc gga gtg gtg gcc gtc tct gtc				2071
Ser Val Leu Arg Ser Pro Met Pro Gly Val Val Val Ala Val Ser Val				
660	665	670	675	
aag cct gga gac gcg gta gca gaa ggt caa gaa att tgt gtg att gaa				2119
Lys Pro Gly Asp Ala Val Ala Glu Gly Gln Glu Ile Cys Val Ile Glu				
676	681	686	691	
gcc atg aaa atg cag aat agt atg aca gct ggg aaa act ggc acg gtg				2167
Ala Met Lys Met Gln Asn Ser Met Thr Ala Gly Lys Thr Gly Thr Val				
692	697	702	707	
aaa tct gtg cac tgt caa gct gga gac aca gtt gga gaa ggg gat ctg				2215
Lys Ser Val His Cys Gln Ala Gly Asp Thr Val Gly Glu Gly Asp Leu				
708	713	718	723	
ctc gtg gag ctg gaa tga aggatt tataacctt cagtcacac ccaatttaat				2269
Leu Val Glu Leu Glu *				
724	729			
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	Met Phe Leu Thr Ser		
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ctc tct agc cct aac cgg cag cca ttt gtt ctc ttt ggt aat cac tcc	401		
Leu Ser Ser Pro Asn Arg Gln Pro Phe Val Leu Phe Gly Asn His Ser			
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aca cga gaa aac ctg aat gct ggc aac ttt aac ttc cct tct gaa gga	449		
Thr Arg Glu Asn Leu Asn Ala Gly Asn Phe Asn Phe Pro Ser Glu Gly			
22	27	32	37
cat ctg gta cga agc act ggt ccc ggc ggg agc ttt gcc aag cac atg	497		
His Leu Val Arg Ser Thr Gly Pro Gly Gly Ser Phe Ala Lys His Met			
38	43	48	53
gta gcc cag tgt gtc tca cca aag gga cct ctt gct tgt tcg aga aca	545		
Val Ala Gln Cys Val Ser Pro Lys Gly Pro Leu Ala Cys Ser Arg Thr			
54	59	64	69
tac ttt ttt gga gct act cat gtt cct tac ttg ggt gac agc aag	593		
Tyr Phe Phe Gly Ala Thr His Val Pro Tyr Leu Gly Gly Asp Ser Lys			
70	75	80	85
ctg ccc aag aaa act gaa caa att agg cta ttg tcc cag ata tat gct	641		
Leu Pro Lys Lys Thr Glu Gln Ile Arg Leu Leu Ser Gln Ile Tyr Ala			
86	91	96	101
gct gtt att gag gct gtt ttg gct ggc att gca tgt tat gct aaa act	689		
Ala Val Ile Glu Ala Val Leu Ala Gly Ile Ala Cys Tyr Ala Lys Thr			
102	107	112	117
tcc agt cta aca aag gcc aag gag gta gca gag caa act ctg gga tct	737		
Ser Ser Leu Thr Lys Ala Lys Glu Val Ala Glu Gln Thr Leu Gly Ser			
118	123	128	133
ggg tta gat tcc ttt gag ttg att ccg ttt aag gca gcc ctg cgc tcc	785		
Gly Leu Asp Ser Phe Glu Leu Ile Pro Phe Lys Ala Ala Leu Arg Ser			
134	139	144	149
aag atg act ttt cat ata cat gct gtg aat aat cag gga aga att gta	833		
Lys Met Thr Phe His Ile His Ala Val Asn Asn Gln Gly Arg Ile Val			
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ccg ctg gac agt gaa gat agc tta tcc ttt gtg aag acg gct tgt atg	881		
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166	171	176	181
gcc gtc tat gac att cct gac tta ctg gga ggc aat ggt tgt tta gga	929		
Ala Val Tyr Asp Ile Pro Asp Leu Leu Gly Gly Asn Gly Cys Leu Gly			
182	187	192	197
tct gtg gtt ttc tct gaa tca ttt ttg act tct cag atc tta gtt aaa	977		
Ser Val Val Phe Ser Glu Ser Phe Leu Thr Ser Gln Ile Leu Val Lys			

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aag tta ctc tca gcc aaa ctc cca gag ctg gac tgg ttt/ctc cag cat Lys Leu Leu Ser Ala Lys Leu Pro Glu Leu Asp Trp Phe Leu Gln His 422 427 432 437				1649

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Phe Ala Ile Ser Ser Ile Ser Gln Glu Pro Val Met Arg Thr His Leu		
438	443	448
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cct gtg ctg ctg cag caa gct gaa atc aac act act cac aga ata gaa		1745
Pro Val Leu Leu Gln Gln Ala Glu Ile Asn Thr Thr His Arg Ile Glu		
454	459	464
469		
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Ser Asp Lys Val Ile Ile Ser Ile Val Thr Gly Leu Pro Gly Cys His		
470	475	480
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Ala Ser Glu Leu Cys Ala Phe Leu Val Thr Leu His Lys Glu Cys Gly		
486	491	496
501		
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Arg Trp Met Val Tyr Arg Gln Ile Met Asp Ser Ser Glu Cys Phe His		
502	507	512
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Asn Arg Ser Ala Arg Gln Ser Ala Tyr Ile Arg Lys Lys Thr Arg Leu		
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Leu Val Val Leu Gln Gly Tyr Thr Asp Val Ile Asp Val Val Gln Ala		
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Leu Gln Thr His Pro Asp Ser Asn Val Lys Ala Ser Phe Thr Ile Gly		
566	571	576
581		
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Ala Ile Thr Ala Cys Val Glu Pro Met Ser Cys Tyr Met Glu His Arg		
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Phe Leu Phe Pro Lys Cys Leu Asp Gln Cys Ser Gln Gly Leu Val Ser		
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Asn Val Val Phe Thr Ser His Thr Thr Glu Gln Arg His Pro Leu Leu		
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661		

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 Lys Pro * 902
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 Ser Leu Val Tyr Ala Gly Ile Lys Ser Ile Val Lys Ser Ser Leu Gly
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 Met Val Glu Ser Ser Arg His Asn Trp Ser Gly Leu Asp Lys Gln Ser
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 Gly Trp Ile Lys Lys Gly Thr Asp Val Asp Val Gly Pro Phe Leu Asn
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 Ser Leu Val Gln Glu Gly Glu Trp Glu Arg Ala Ala Ala Val Ala Leu
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 Phe Asn Leu Asp Ile Arg Arg Ala Ile Gln Ile Leu Asn Glu Gly Ala
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 123 128 133 138
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 139 144 149 154

ttt ctg aca agt gaa aca gga tct tac gat gga gtt ttg tat gaa aac Phe Leu Thr Ser Glu Thr Gly Ser Tyr Asp Gly Val Leu Tyr Glu Asn 155 160 165 170	591
aaa gtt gca gta cgt gac aga gtg gca ttt gct tgt aaa ttc ctt agt Lys Val Ala Val Arg Asp Arg Val Ala Phe Ala Cys Lys Phe Leu Ser 171 176 181 186	639
gat act cag tta aat aga tac atc gaa aag ttg acc aat gaa atg aaa Asp Thr Gln Leu Asn Arg Tyr Ile Glu Lys Leu Thr Asn Glu Met Lys 187 192 197 202	687
gag gct gga aat ttg gaa gga att ttg ctt aca ggc ctt act aaa gat Glu Ala Gly Asn Leu Glu Gly Ile Leu Leu Thr Gly Leu Thr Lys Asp 203 208 213 218	735
gga gtg gac tta atg gag agt tat gtt gat aga act gga gat gtt caa Gly Val Asp Leu Met Glu Ser Tyr Val Asp Arg Thr Gly Asp Val Gln 219 224 229 234	783
aca gca agt tac tgt atg tta cag ggt tca cct tta gat gtt ctt aaa Thr Ala Ser Tyr Cys Met Leu Gln Gly Ser Pro Leu Asp Val Leu Lys 235 240 245 250	831
gat gaa agg gtt cag tac tgg att gag aat tat aga aat tta tta gat Asp Glu Arg Val Gln Tyr Trp Ile Glu Asn Tyr Arg Asn Leu Leu Asp 251 256 261 266	879
gcc tgg agg ttt tgg cat aaa cga gct gaa ttt gat att cac agg agt Ala Trp Arg Phe Trp His Lys Arg Ala Glu Phe Asp Ile His Arg Ser 267 272 277 282	927
aag ttg gat ccc agt tcc aag cct tta gca caa gtt ttt gtg agt tgc Lys Leu Asp Pro Ser Ser Lys Pro Leu Ala Gln Val Phe Val Ser Cys 283 288 293 298	975
aat ttc tgt ggc aag tca atc tcc tac agc tgt tca gct gtg cct cat Asn Phe Cys Gly Lys Ser Ile Ser Tyr Ser Cys Ser Ala Val Pro His 299 304 309 314	1023
cag ggc aga ggt ttt agt cag tat ggt gtg agt ggc tca cca acg aaa Gln Gly Arg Gly Phe Ser Gln Tyr Gly Val Ser Gly Ser Pro Thr Lys 315 320 325 330	1071
tct aaa gtc aca agt tgt cct ggc tgt cga aaa cca ctt cct cga tgt Ser Lys Val Thr Ser Cys Pro Gly Cys Arg Lys Pro Leu Pro Arg Cys 331 336 341 346	1119
gcg ctt tgt ctc att aat atg gga aca cca gtt tct agc tgt cct gga Ala Leu Cys Leu Ile Asn Met Gly Thr Pro Val Ser Ser Cys Pro Gly 347 352 357 362	1167
gga acc aaa tca gat gaa aaa gtg gac ttg agc aag gac aaa aaa tta Gly Thr Lys Ser Asp Glu Lys Val Asp Leu Ser Lys Asp Lys Lys Leu 363 368 373 378	1215

gcc caa ttt aac aac tgg ttt aca tgg tgt cat aat tgc agg cac ggt Ala Gln Phe Asn Asn Trp Phe Thr Trp Cys His Asn Cys Arg His Gly 379 384 389 394	1263
gga cat gct gga cat atg ctt agt tgg ttc agg gac cat gca gag tgc Gly His Ala Gly His Met Leu Ser Trp Phe Arg Asp His Ala Glu Cys 395 400 405 410	1311
cct gtg tct gca tgc acg tgt aaa tgt atg cag ttg gat aca acg ggg Pro Val Ser Ala Cys Thr Cys Lys Cys Met Gln Leu Asp Thr Thr Gly 411 416 421 426	1359
aat ctg gta cct gca gag act gtc cag cca taa aatgttac cacccttaaga Asn Leu Val Pro Ala Glu Thr Val Gln Pro * 427 432 437	1410
gaacccttca agtgtggagc tttctagtag gtgtccttca tagctcagaa acatacctca	1470
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aaaaaaaa	1537

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 <213> Homo sapiens

<220>
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 <222> (148)..(615)

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actccagaat tggccgctgg cggtatac atg gcg acc cgg aac ccc cct ccc Met Ala Thr Arg Asn Pro Pro Pro 1 5	171
caa gac tat gaa agt gat gac gac tct tat gaa gtg ttg gat tta act Gln Asp Tyr Glu Ser Asp Asp Ser Tyr Glu Val Leu Asp Leu Thr 9 14 19 24	219
gag tat gca aga aga cac cag tgg tgg aat cga gtg ttt ggc cac agt Glu Tyr Ala Arg Arg His Gln Trp Trp Asn Arg Val Phe Gly His Ser 25 30 35 40	267
tcg gga cct atg gta gaa aaa tac tca gta gct acc cag att gta atg Ser Gly Pro Met Val Glu Lys Tyr Ser Val Ala Thr Gln Ile Val Met 41 46 51 56	315
ggt ggc gtt act ggc tgg tgt gca gga ttt ctg ttc cag aaa gtt gga Gly Gly Val Thr Gly Trp Cys Ala Gly Phe Leu Phe Gln Lys Val Gly	363

57	62	67	72	
aaa ctt gca gca act gca gta ggt ggt ggc ttt ctt ctt ctt cag att				411
Lys Leu Ala Ala Thr Ala Val Gly Gly Gly Phe Leu Leu Leu Gln Ile				
73	78	83	88	
gct agt cat agt ggc tat gtg cag att gac tgg aag aga gtt gaa aaa				459
Ala Ser His Ser Gly Tyr Val Gln Ile Asp Trp Lys Arg Val Glu Lys				
89	94	99	104	
gat gta aat aaa gca aaa aga cag att aag aaa cga gcg aac aaa gca				507
Asp Val Asn Lys Ala Lys Arg Gln Ile Lys Lys Arg Ala Asn Lys Ala				
105	110	115	120	
gca cct gaa atc aac aat tta att gaa gaa gca aca gaa ttt atc aag				555
Ala Pro Glu Ile Asn Asn Leu Ile Glu Glu Ala Thr Glu Phe Ile Lys				
121	126	131	136	
cag aac att gtg ata tcc agt gga ttt gtg gga ggc ttt ttg ctc gga				603
Gln Asn Ile Val Ile Ser Ser Gly Phe Val Gly Gly Phe Leu Leu Gly				
137	142	147	152	
ctt gca tct taa gga catgaatatt ctcccataac ggattcaact atgagaagag				658
Leu Ala Ser *				
153				
aagtggcagc aataaggcag tctctcaaaa gtcatactgc cagagtctct agggcaagga				718
gaaacaacta gctggacaat actcaattca caacttagca ttttgcacatc tgaagcttgg				778
caaactagta tctgctgtaa aacaacctat atggatgtg aaccgttagta ttcctgagca				838
aaacgtggct ttcatcgctt tgtaaaaatt tgcattgtt tagaaaactag cctataaaat				898
atcaccattt gatgttagata tggagagaaa agaaaatatgt tgggtttatt gcttagcgaa				958
atattctctt tttatattaaa taaaatgttc ttcattgtgt tttatggat gtgtccataa				1018
tttaaaaattc atgttatagt ttcagtattt aggctgactt tttttttta agatatgttt				1078
gcaataagtt aaaaaactgt aatacccttt tggaaagc ttttagaaatg atataattat				1138
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 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (14) .. (787)

<400> 563

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	Met	Ala	Thr	His	Gly	Gly	Ser	Arg	Leu	Asn	Leu	Ser					
	1				5				10								
													/				
ttg	gta	ccg	agc	tcg	gat	cca	cta	gtc	cag	tgt	ggt	gga	att	cac	aaa	97	
Leu	Val	Pro	Ser	Ser	Asp	Pro	Leu	Val	Gln	Cys	Gly	Ile	His	Lys			
13					18				23			28					
gga	gcg	gcf	gcc	ggg	agc	gga	ctt	acc	tta	cct	tct	ctg	cct	tcg	gcf	145	
Gly	Ala	Ala	Ala	Gly	Ser	Gly	Leu	Thr	Leu	Pro	Ser	Leu	Pro	Ser	Ala		
29					34				39			44					
cgc	tcc	tca	gcc	ggg	ccg	ccg	acc	caa	agg	agg	agc	cgt	ccg	act	atg	tct	193
Arg	Phe	Ser	Ala	Gly	Pro	Pro	Thr	Gln	Arg	Ser	Arg	Pro	Thr	Met	Ser		
45					50				55			60					
aac	atg	gag	aaa	cac	ctg	ttc	aac	ctg	aag	ttc	gcf	gcc	aaa	gaa	ctg	241	
Asn	Met	Glu	Lys	His	Leu	Phe	Asn	Leu	Lys	Phe	Ala	Ala	Lys	Glu	Leu		
61					66				71			76					
agt	agg	agt	gcc	aaa	aaa	tgc	gat	aag	gag	gaa	aag	gcc	gaa	aag	gcc	289	
Ser	Arg	Ser	Ala	Lys	Lys	Cys	Asp	Lys	Glu	Glu	Lys	Ala	Glu	Lys	Ala		
77					82				87			92					
aaa	att	aaa	aag	gcc	att	cag	aag	ggc	aac	atg	gaa	gtt	gcf	agg	ata	337	
Lys	Ile	Lys	Lys	Ala	Ile	Gln	Lys	Gly	Asn	Met	Glu	Val	Ala	Arg	Ile		
93					98				103			108					
cac	gcc	gaa	aat	gcc	atc	cgc	cag	aag	aac	cag	gcf	gtg	aat	ttc	ttg	385	
His	Ala	Glu	Asn	Ala	Ile	Arg	Gln	Lys	Asn	Gln	Ala	Val	Asn	Phe	Leu		
109					114				119			124					
aga	atg	agt	gcf	cga	gtc	gat	gca	gtg	gct	gcc	agg	gtc	cag	acg	gcf	433	
Arg	Met	Ser	Ala	Arg	Val	Asp	Ala	Val	Ala	Ala	Arg	Val	Gln	Thr	Ala		
125					130				135			140					
gtg	acg	atg	ggc	aag	gtg	acc	aag	tcg	atg	gct	ggt	gtg	gtt	aag	tcg	481	
Val	Thr	Met	Gly	Lys	Val	Thr	Lys	Ser	Met	Ala	Gly	Val	Val	Lys	Ser		
141					146				151			156					
atg	gat	gcf	aca	ttg	aag	acc	atg	aat	ctg	gag	aag	att	tct	gct	ttg	529	
Met	Asp	Ala	Thr	Leu	Lys	Thr	Met	Asn	Leu	Glu	Lys	Ile	Ser	Ala	Leu		
157					162				167			172					
atg	gac	aaa	ttc	gag	cac	cag	ttt	gag	act	ctg	gac	gtc	cag	acg	cag	577	
Met	Asp	Lys	Phe	Gl	His	Gln	Phe	Gl	Thr	Leu	Asp	Val	Gln	Thr	Gln		
173					178				183			188					
caa	atg	gaa	gac	acg	atg	agc	agc	acg	acg	ctc	acc	act	ccc	cag	625		
Gln	Met	Glu	Asp	Thr	Met	Ser	Ser	Thr	Thr	Leu	Thr	Thr	Pro	Gln			
189					194				199			204					
aac	caa	gtg	gat	atg	ctg	ctc	cag	gaa	atg	gca	gat	gag	gcf	ggc	ctc	673	
Asn	Gln	Val	Asp	Met	Leu	Leu	Gln	Met	Ala	Asp	Glu	Ala	Gly	Leu			
205					210				215			220					
gac	ctc	aac	atg	gag	ctg	ccg	cag	ggc	cag	acc	ggc	tcc	gtg	ggc	acg	721	

Asp	Leu	Asn	Met	Glu	Leu	Pro	Gln	Gly	Gln	Thr	Gly	Ser	Val	Gly	Thr	
221					226				231				236			
agc	gtg	gct	tcg	gcg	gag	cag	gat	gaa	ctg	tct	cag	aga	ctg	gcc	cgc	769
Ser	Val	Ala	Ser	Ala	Glu	Gln	Asp	Glu	Leu	Ser	Gln	Arg	Leu	Ala	Arg	
237					242				247				252			
ctt	cgg	gat	caa	gtg	tga	cgccag	aacccgctct	gaggttcct	ggccatagcc							823
Leu	Arg	Asp	Gln	Val	*											
253					258											
acc	ctt	gaa	atg	ctc	tct	tgt	gtt	tagag	agata	actata	cc	ct	aga	aa	ac	883
cc	aga	atg	ct	cc	ct	t	tt	ac	tg	tt	cc	cc	ca	ca	ca	943
a	att	c	tc	tc	tc	t	t	tc	t	aa	tt	tt	aa	tt	aa	1003
t	at	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1063
tt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1123
tt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1183
aa	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	ag	1243
cg	gt	gg	ac	tg	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1303
ct	tc	ac	at	gt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1363
t	ata	att	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1423
t	t	c	ta	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1483
t	c	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1543
t	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1603
t	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1663
t	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	1723
cc	ct	tt	gg	ac	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1783
at	ta	tt	gg	aa	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1843
tt	gg	aa	at	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1903
at	ac	at	cc	ag	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	1963
gt	tt	gg	ac	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2023
tg	cg	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2083
at	gg	aa	aa	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	2143
tt	tt	ta	cc	tt	tt	cc	tt	cc	tt	cc	tt	cc	tt	cc	tt	2203

agaaaataat tataggggcc cttccaagtt ctttcaaaga ttcataacca actattca	2263
attataacat gtttcccagt gtaaatgagt aaggaaaaaa aaagtgtaac aggtgcgtgc	2323
agatgaggag tgaccctcat atttaagttt ttttatattt gactggacat tgttcagaag	2383
tgtgctttaa gggacacttg ttgggtgtct gcccagcatc tctcaagaat atccctcctg	2443
tcctccacat ggttgcag ggccatgtgt gaagacagca tgagtcttaa cccctctttt	2503
attttatttt tgagacagag tctcgctctg ttgcccaggc tggagtgtgc tggcgcgatc	2563
tctgctcaact gcaaccccca cctccgggt tcaagtgatt ctccctgcctc agcctgccga	2623
gtagctggaa ttacaggtgt gcaccacca gcccagctag ttttttgtta tttttagtag	2683
agacagggtt tcactatgtt ggccaggctg gtcttgaact cctgacctca ggtgatccgc	2743
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ccctcttttag attggaaaaaa ataattacaa cttaaaaat agcttagtgt tgaacccttt	2863
ggtaaactaa agaccctttt ataatgcaca tattcccaac aaaattaata tattttgtga	2923
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ttttttttt tttttgaatg tgagccaaag atttatttct tcatttcttgc cattgaaat	180
actcttcaat gacatccttgc gcctgagact ccttgcata gtccttaact actacacaac	240
tgcaaccaac cacttacgg gttttccctt ctctgtcaat tttacaaagg cttacccatt	300
ctcctagttt cttgttgtca tcaaccttaa tttaggttgc ttgggtttca gcacaaaggg	360
cctccaccaa cttgacatac ataggctcat cacagtttgc tgcaagcaca caaagatggg	420
cttggcgctt gtcttaaggct ttggcagctt cgcgaattcc acgtgcttagg ccatcgttgc	480

tgagggcagt	cttcagaacc	tcttgtaaag	cagtattaac	gtccattaca	cctccagcag	540										
caatgccttc	ctcgccca	tgg	cgg	tgg	gtt	acg	ggt	gaa	gct	gaa	tct	tga	591			
		Met	Ala	Glu	Glu	Gly	Ile	Ala	Ala	Gly	Gly	Val				
		1					5									
acg	cac	cca	agc	ctc	cgc	ctc	cgc	gct	act	cgg	cgg	cat	tac	tag	tga	639
Met	Asp	Val	Asn	Thr	Ala	Leu	Gln	Glu	Val	Leu	Lys	Thr	Ala	Leu	Ile	
12							17			22				27		
tta	cta	gtg	aat	tca	cta	gta	ata	tta	cta	gtg	aat	cac	tag	taa	tat	687
His	Asp	Gly	Leu	Ala	Arg	Gly	Ile	Arg	Glu	Ala	Ala	Lys	Ala	Leu	Asp	
28							33			38				43		
tac	tag	tga	att	cac	tag	taa	tgt	cgc	gct	gag	gct	gag	gct	tgg	gtg	735
Lys	Arg	Gln	Ala	His	Leu	Cys	Val	Leu	Ala	Ser	Asn	Cys	Asp	Glu	Pro	
44							49			54				59		
cgt	tca	aga	ttc	agc	ttc	acc	cgt	aac	cca	ccg	cca	tgg	ccg	agg	aag	783
Met	Tyr	Val	Lys	Leu	Val	Glu	Ala	Leu	Cys	Ala	Glu	His	Gln	Ile	Asn	
60							65			70				75		
gca	ttg	ctg	ctg	gag	gtg	taa	tgg	acg	tta	ata	ctg	ctt	tac	aag	agg	831
Leu	Ile	Lys	Val	Asp	Asp	Asn	Lys	Lys	Leu	Gly	Glu	Trp	Val	Gly	Leu	
76							81			86				91		
ttc	tga	aga	ctg	ccc	tca	tcc	acg	atg	gcc	tag	cac	gtg	gaa	ttc	gct	879
Cys	Lys	Ile	Asp	Arg	Glu	Gly	Lys	Pro	Arg	Lys	Val	Val	Gly	Cys	Ser	
92							97			102				107		
aag	ctg	cca	aag	cct	tag	aca	agc	gcc	aag	ccc	atc	ttt	gtg	tgc	ttg	927
Cys	Val	Val	Val	Lys	Asp	Tyr	Gly	Lys	Ser	Gln	Ala	Lys	Asp	Val		
108							113			118				123		
cat	cca	act	gtg	atg	agc	cta	tgt	atg	tca	a	gttggtag	gttggtag	gttggtag	gttggtag	gttggtag	978
Ile	Glu	Glu	Tyr	Phe	Lys	Cys	Lys	Lys	*							
124							129									
ctgaacacca	aatcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	atcaaccta	1038
gcctttgtaa	aattgacaga	gagggaaac	cccgtaaagt	ggttggtag	agttgtgttag											1098
tagtttaagga	ctatggcaag	gagtctcagg	ccaaggatgt	cattgaagag	tatttcaaat											1158
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Met Thr Lys Asn Asp Ala Pro Ala Leu Val			
1	5		
att aca aca caa tgt gaa att tgc tat aaa ggt aac ctt gaa aat agt	160		
Ile Thr Thr Gln Cys Glu Ile Cys Tyr Lys Gly Asn Leu Glu Asn Ser			
11	16	21	26
aca atg act gct gcc att aaa gat ctc caa gtg aga gcc tgc ccg ttt	208		
Thr Met Thr Ala Ala Ile Lys Asp Leu Gln Val Arg Ala Cys Pro Phe			
27	32	37	42
ctt cca gtc aag aga aaa ggc aaa atc act act gtt ttg cag ccc tgt	256		
Leu Pro Val Lys Arg Lys Gly Lys Ile Thr Thr Val Leu Gln Pro Cys			
43	48	53	58
gac ttg ttt tat caa act act cag aaa ggt aca gat cca caa gtg atc	304		
Asp Leu Phe Tyr Gln Thr Thr Gln Lys Gly Thr Asp Pro Gln Val Ile			
59	64	69	74
gat atg tca gta aaa tcc ctg aca cta aag gtt tca cca gtt att ata	352		
Asp Met Ser Val Lys Ser Leu Thr Leu Lys Val Ser Pro Val Ile Ile			
75	80	85	90
aat act atg att acc ata act tca gca ctg tat aca act aag gaa acc	400		
Asn Thr Met Ile Thr Ser Ala Leu Tyr Thr Thr Lys Glu Thr			
91	96	101	106
atc cca gaa gaa acg gct tct act gca cat tta tgg gaa aag aag	448		
Ile Pro Glu Glu Thr Ala Ser Ser Thr Ala His Leu Trp Glu Lys Lys			
107	112	117	122
gat aca aag act tta aaa atg tgg ttt ctt gaa gaa tca aat gaa act	496		
Asp Thr Lys Thr Leu Lys Met Trp Phe Leu Glu Glu Ser Asn Glu Thr			
123	128	133	138
gaa aaa ata gct ccc aca act gaa ttg gta ccc aaa ggc gag atg ata	544		
Glu Lys Ile Ala Pro Thr Thr Glu Leu Val Pro Lys Gly Glu Met Ile			
139	144	149	154
aaa atg aac att gat tct att ttt ata gtt ctt gag gct gga att ggt	592		
Lys Met Asn Ile Asp Ser Ile Phe Ile Val Leu Glu Ala Gly Ile Gly			
155	160	165	170
cat aga aca gta cct atg ctt ctg gca aag tca cgt ttt tca ggg gaa	640		
His Arg Thr Val Pro Met Leu Leu Ala Lys Ser Arg Phe Ser Gly Glu			
171	176	181	186
ggc aaa aac tgg agt tcc cta ata aat ctg cac tgt cag ctt gag cta	688		
Gly Lys Asn Trp Ser Ser Leu Ile Asn Leu His Cys Gln Leu Glu Leu			
187	192	197	202
gaa gtg cat tat tat aat gaa atg ttt ggt gta tgg gag cct ttg ctt	736		

Glu	Val	His	Tyr	Tyr	Asn	Glu	Met	Phe	Gly	Val	Trp	Glu	Pro	Leu	Leu	
203						208					213			218		
gaa ccc tta gaa att gat cag act gag gat ttt aga cca tgg aat ctt															784	
Glu	Pro	Leu	Glu	Ile	Asp	Gln	Thr	Glu	Asp	Phe	Arg	Pro	Trp	Asn	Leu	
219						224				229			234			
ggt atc aag atg aaa aag aaa gca aaa atg gcc att gtt gag tca gat															832	
Gly	Ile	Lys	Met	Lys	Lys	Ala	Lys	Met	Ala	Ile	Val	Glu	Ser	Asp		
235						240			245			250				
cct gaa gaa gaa aac tac aaa gtg cca gaa tat aaa act gtc atc agt															880	
Pro	Glu	Glu	Asn	Tyr	Lys	Val	Pro	Glu	Tyr	Lys	Thr	Val	Ile	Ser		
251						256			261			266				
ttc cat tca aaa gac caa tta aac att aca tta tcc aaa tgt ggt ctt															928	
Phe	His	Ser	Lys	Asp	Gln	Leu	Asn	Ile	Thr	Leu	Ser	Lys	Cys	Gly	Leu	
267						272			277			282				
gta atg tta aac aat tta gtc aag gca ttt aca gaa gct gcc act gga															976	
Val	Met	Leu	Asn	Asn	Leu	Val	Lys	Ala	Phe	Thr	Glu	Ala	Ala	Thr	Gly	
283						288			293			298				
tct tca gct gac ttc gta aag gat cta gca cca ttt atg att tta aat															1024	
Ser	Ser	Ala	Asp	Phe	Val	Lys	Asp	Leu	Ala	Pro	Phe	Met	Ile	Leu	Asn	
299						304			309			314				
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Ser	Leu	Gly	Leu	Thr	Ile	Ser	Val	Ser	Pro	Ser	Asp	Ser	Phe	Ser	Val	
315						320			325			330				
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331						336			341			346				
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Leu	Ser	Met	Asp	Tyr	Ile	Arg	Thr	Lys	Asp	Asn	Asp	His	Phe	Asn	Ala	
347						352			357			362				
atg acc agc cta agc agc aaa ctc ttc att ctt ctt aca cct gtt															1216	
Met	Thr	Ser	Leu	Ser	Ser	Lys	Leu	Phe	Phe	Ile	Leu	Leu	Thr	Pro	Val	
363						368			373			378				
aac cat tct act gct gat aag att cct tta aca aaa gtg gga cga cgt															1264	
Asn	His	Ser	Thr	Ala	Asp	Lys	Ile	Pro	Leu	Thr	Lys	Val	Gly	Arg	Arg	
379						384			389			394				
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Leu	Tyr	Thr	Val	Arg	His	Arg	Glu	Ser	Gly	Val	Glu	Arg	Ser	Ile	Val	
395						400			405			410				
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Cys	Gln	Ile	Asp	Thr	Val	Glu	Gly	Ser	Lys	Lys	Val	Thr	Ile	Arg	Ser	
411						416			421			426				
cca gtg cag ata aga aat cat ttt tca gtc cca ctg tct gtt tac gaa															1408	
Pro	Val	Gln	Ile	Arg	Asn	His	Phe	Ser	Val	Pro	Leu	Ser	Val	Tyr	Glu	

427	432	437	442	
ggg gat acc tta ttg gga act gcc tca cct gaa aat gaa ttc aac ata Gly Asp Thr Leu Leu Gly Thr Ala Ser Pro Glu Asn Glu Phe Asn Ile				1456
443	448	453	458	
cca tta gga tct tac cga tca ttc att ttt ctg aag cca gaa gat gag Pro Leu Gly Ser Tyr Arg Ser Phe Ile Phe Leu Lys Pro Glu Asp Glu				1504
459	464	469	474	
aac tat caa atg tgt gaa gga att gac ttt gaa gag att ata aaa aat Asn Tyr Gln Met Cys Glu Gly Ile Asp Phe Glu Glu Ile Ile Lys Asn				1552
475	480	485	490	
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491	496	501	506	
gaa tca ttt ctc att aat att gtt cca gaa aaa gat aat tta aca tct Glu Ser Phe Leu Ile Asn Ile Val Pro Glu Lys Asp Asn Leu Thr Ser				1648
507	512	517	522	
cta tca gtg tat tca gaa gat ggt tgg gat tta cca tac ata atg cat Leu Ser Val Tyr Ser Glu Asp Gly Trp Asp Leu Pro Tyr Ile Met His				1696
523	528	533	538	
ttg tgg cca cct atc ctg ctc cga aat ctt ctt cct tac aaa att gct Leu Trp Pro Pro Ile Leu Leu Arg Asn Leu Leu Pro Tyr Lys Ile Ala				1744
539	544	549	554	
tat tat ata gag gga att gaa aat tcg gtt ttt act cta agt gaa gga Tyr Tyr Ile Glu Gly Ile Glu Asn Ser Val Phe Thr Leu Ser Glu Gly				1792
555	560	565	570	
cat tca gcc cag att tgt act gca cag ttg ggt aaa gcc agg cta cat His Ser Ala Gln Ile Cys Thr Ala Gln Leu Gly Lys Ala Arg Leu His				1840
571	576	581	586	
tta aaa tta ctt gac tat ctc aat cac gat tgg aaa agt gaa tat cac Leu Lys Leu Leu Asp Tyr Leu Asn His Asp Trp Lys Ser Glu Tyr His				1888
587	592	597	602	
ata aag cct aat cag caa gac att agt ttt gtc agt ttt act tgt gtt Ile Lys Pro Asn Gln Gln Asp Ile Ser Phe Val Ser Phe Thr Cys Val				1936
603	608	613	618	
aca gaa atg gaa aag act gat tta gat att gct gtc cat atg act tac Thr Glu Met Glu Lys Thr Asp Leu Asp Ile Ala Val His Met Thr Tyr				1984
619	624	629	634	
aat act ggt cag aca gtt gtg gca ttt cat agt cct tat tgg atg gtc Asn Thr Gly Gln Thr Val Val Ala Phe His Ser Pro Tyr Trp Met Val				2032
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651	656	661	666	

aag cat cca cct aat tat aaa aag cca gtt ctc ttt tct ttt cag cca Lys His Pro Pro Asn Tyr Lys Lys Pro Val Leu Phe Ser Phe Gln Pro 667 672 677 682	2128
aat cac ttt ttt aat aac aat aag gtt caa ctt atg gta act gat agt Asn His Phe Phe Asn Asn Asn Lys Val Gln Leu Met Val Thr Asp Ser 683 688 693 698	2176
gag ttg tcc aat cag ttt tca att gat act gtt ggt agt cat gga gct Glu Leu Ser Asn Gln Phe Ser Ile Asp Thr Val Gly Ser His Gly Ala 699 704 709 714	2224
gtt aaa tgt aaa ggc ctg aaa atg gac tat caa gtt ggt gtc act ata Val Lys Cys Lys Gly Leu Lys Met Asp Tyr Gln Val Gly Val Thr Ile 715 720 725 730	2272
gac ctg agc agt ttt aac att act aga att gtg aca ttt acc cct ttt Asp Leu Ser Ser Phe Asn Ile Thr Arg Ile Val Thr Phe Thr Pro Phe 731 736 741 746	2320
tat atg att aaa aac aaa agc aaa tac cat ata tca gtg gct gaa gaa Tyr Met Ile Lys Asn Lys Ser Lys Tyr His Ile Ser Val Ala Glu Glu 747 752 757 762	2368
gga aat gat aaa tgg ctc tct ctt gat ttg gag cag tgt atc ccc ttt Gly Asn Asp Lys Trp Leu Ser Leu Asp Leu Glu Gln Cys Ile Pro Phe 763 768 773 778	2416
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gaa gat cct ccc aaa agg ata tat ttt aac aag cag gaa aat tgt att Glu Asp Pro Pro Lys Arg Ile Tyr Phe Asn Lys Gln Glu Asn Cys Ile 795 800 805 810	2512
cta ttg cgt cta gat aac gag ctt gga ggt att ata gca gaa gtg aat Leu Leu Arg Leu Asp Asn Glu Leu Gly Gly Ile Ile Ala Glu Val Asn 811 816 821 826	2560
ttg gcc gag cat tct aca gtt att aca ttt tta gat tat cat gat gga Leu Ala Glu His Ser Thr Val Ile Thr Phe Leu Asp Tyr His Asp Gly 827 832 837 842	2608
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gta ttt aaa gta aca tat gaa agt gag aaa gca gag tta gca gag caa Val Phe Lys Val Thr Tyr Glu Ser Glu Lys Ala Glu Leu Ala Glu Gln 939 944 949 954	2944
gaa att gca gtg gca tta caa gat gtt gga att tct ctt gtc aac aat Glu Ile Ala Val Ala Leu Gln Asp Val Gly Ile Ser Leu Val Asn Asn 955 960 965 970	2992
tac acg aag caa gaa gta gcc tat ata ggc att aca agt tct gat gtg Tyr Thr Lys Gln Glu Val Ala Tyr Ile Gly Ile Thr Ser Ser Asp Val 971 976 981 986	3040
gtt tgg gaa aca aag ccc aag aag aag gca aga tgg aag cca atg agt Val Trp Glu Thr Lys Pro Lys Lys Ala Arg Trp Lys Pro Met Ser 987 992 997 1002	3088
gta aag cac act gag aag tta gag aga gaa ttt aag gaa tat act gaa Val Lys His Thr Glu Lys Leu Glu Arg Glu Phe Lys Glu Tyr Thr Glu 1003 1008 1013 1018	3136
tct tct cct tca gaa gat aag gtt att cag ttg gac act aat gtt ccg Ser Ser Pro Ser Glu Asp Lys Val Ile Gln Leu Asp Thr Asn Val Pro 1019 1024 1029 1034	3184
gtt cgc cta acc cct act ggt cat aac atg aaa att ctg cag ccg cat Val Arg Leu Thr Pro Thr Gly His Asn Met Lys Ile Leu Gln Pro His 1035 1040 1045 1050	3232
gta ata gct cta cga aga aat tat ctt cca gca tta aaa gtg gaa tat Val Ile Ala Leu Arg Arg Asn Tyr Leu Pro Ala Leu Lys Val Glu Tyr 1051 1056 1061 1066	3280
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1147						1152				1157				1162	
gag gtg act gaa aat aca gag gtt gag ctt ttt cat aaa gat ata gaa														3616	
Glu	Val	Thr	Glu	Asn	Thr	Glu	Val	Glu	Leu	Phe	His	Lys	Asp	Ile	Glu
1163						1168				1173				1178	
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Ala	Phe	Lys	Glu	Glu	Tyr	Lys	Thr	Ala	Ser	Leu	Val	Asp	Gln	Ser	Gln
1179						1184				1189				1194	
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Val	Ser	Leu	Tyr	Glu	Tyr	Phe	His	Ile	Ser	Pro	Ile	Lys	Leu	His	Leu
1195						1200				1205				1210	
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Ser	Val	Ser	Leu	Ser	Ser	Gly	Arg	Glu	Glu	Ala	Lys	Asp	Ser	Lys	Gln
1211						1216				1221				1226	
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1227						1232				1237				1242	
att ggt gcc aca ctg aca gat gta caa gat gta gtt ttt aag ctt gca														3856	
Ile	Gly	Ala	Thr	Leu	Thr	Asp	Val	Gln	Asp	Val	Val	Phe	Lys	Leu	Ala
1243						1248				1253				1258	
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1275						1280				1285				1290	
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1291						1296				1301				1306	
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1307						1312				1317				1322	
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Lys	Ala	Leu	Val	Gly	Gly	Ala	Val	Gly	Gly	Leu	Ala	Gly	Ala	Ala	Ser

1339	1344	1349	1354	
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Glu Asp Tyr Gln Gln Lys Arg Arg Glu Ala Met Asn Lys Gln Pro Ala				
1371	1376	1381	1386	
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Gly Phe Arg Glu Gly Ile Thr Arg Gly Gly Lys Gly Leu Val Ser Gly				
1387	1392	1397	1402	
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Phe Val Ser Gly Ile Thr Gly Ile Val Thr Lys Pro Ile Lys Gly Ala				
1403	1408	1413	1418	
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Gln Lys Gly Gly Ala Ala Gly Phe Phe Lys Gly Val Gly Lys Gly Leu				
1419	1424	1429	1434	
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Val Gly Ala Val Ala Arg Pro Thr Gly Gly Ile Ile Asp Met Ala Ser				
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Ser Thr Phe Gln Gly Ile Lys Arg Ala Thr Glu Thr Ser Glu Val Glu				
1451	1456	1461	1466	
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Ser Leu Arg Pro Pro Arg Phe Phe Asn Glu Asp Gly Val Ile Arg Pro				
1467	1472	1477	1482	
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Tyr Arg Leu Arg Asp Gly Thr Gly Asn Gln Met Leu Gln Lys Ile Gln				
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Phe Tyr Arg Glu Trp Ile Met Thr His Ser Ser Ser Asp Asp Asp				
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Asp Asp Asp Asp Asp Asp Glu Ser Asp Leu Asn His *				
1515	1520	1525		
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gcccatatgt ccatttatag ggaggtaaaa cacattttct tttaaatgt ttccctacac				4793
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5078

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cgaaggacgc cgccgggagc tgccggagcat gcgtggagtgcagtgctaa cggctggtgt 240

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Met Ala Gly
1

aag ggg tca tca ggc agg cgg ccc ctg ctg ctg ggg ctg ctg gtg gcc 342
Lys Gly Ser Ser Gly Arg Arg Pro Leu Leu Leu Gly Leu Leu Val Ala
4 9 14 19

gta gcc act gtc cac ctg gtc atc tgt ccc tac acc aaa gtg gag gag 390
Val Ala Thr Val His Leu Val Ile Cys Pro Tyr Thr Lys Val Glu Glu
20 25 30 35

agc ttc aac ctg cag gcc aca cat gac ctg ctc tac cac tgg caa gac 438
Ser Phe Asn Leu Gln Ala Thr His Asp Leu Leu Tyr His Trp Gln Asp
36 41 46 51

ctg gag cag tac gac cat ctt gag ttc ccc gga gtc gtc ccc agg acg 486
Leu Glu Gln Tyr Asp His Leu Glu Phe Pro Gly Val Val Pro Arg Thr
52 57 62 67

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Phe Leu Gly Pro Val Val Ile Ala Val Phe Ser Ser Pro Ala Val Tyr
68 73 78 83

gtg ctt tcg ctg tta gaa atg tcc aag ttt tac tct cag cta ata gtt 582
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84 89 94 99

aga gga gtg ctt gga ctc ggc gtg att ttt gga ctc tgg acg tta caa	630
Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp Thr Leu Gln	
100 105 110 115	
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Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr Met Phe Cys	
116 121 126 131	
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Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys Thr Arg Thr	
132 137 142 147	
ctg ccc aat gtg ctg gcc ctg cct gta gtc ctg ctg gcc ctc gcg gcc	774
Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala Leu Ala Ala	
148 153 158 163	
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Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser Ala Phe Ala	
164 169 174 179	
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Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly Leu Leu Leu	
180 185 190 195	
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Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg Ala Leu Arg	
196 201 206 211	
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His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr Val Ala Val	
212 217 222 227	
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Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly Lys Val Leu	
228 233 238 243	
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Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly Thr Ser Pro	
244 249 254 259	
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Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr His Ala Pro	
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Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu Leu Pro His	
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Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu Asn Ile Thr	
308 313 318 323	
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Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys Lys Ser Trp				
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Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu Val Val Asn				
340	345	350	355	
gcc gcc tac tca gcc acg gcc ctg tat gtg tcc cat ttc aac tac cca				1398
Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe Asn Tyr Pro				
356	361	366	371	
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Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro Pro Gln Thr				
372	377	382	387	
gac gtc ctt ctg cac att gac gtg gca gcc gcc cag aca ggt gtg tct				1494
Asp Val Leu Leu His Ile Asp Val Ala Ala Gln Thr Gly Val Ser				
388	393	398	403	
cggtttctcaaa gtc aac agc gcc tgg agg tac gac aag agg gag gat				1542
Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys Arg Glu Asp				
404	409	414	419	
gtgcagccgggaca ggc atg ctg gca tac aca cac atc ctc atg gag				1590
Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile Leu Met Glu				
420	425	430	435	
gcg gcc cct ggg ctc ctg gcc ctc tac agg gac aca cac cgg gtc ctg				1638
Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His Arg Val Leu				
436	441	446	451	
gcc agc gtc gtg ggg acc aca ggt gtg agt ctg aac ctg acc caa ctg				1686
Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu Thr Gln Leu				
452	457	462	467	
ccc ccc ttc aac gtc cac ctg cag aca aag ctg gtg ctt ctg gag agg				1734
Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu Leu Glu Arg				
468	473	478	483	
ctc ccc cgg ccg tcc tga gggggccatcaggcagccatcaggcagccatcaggccttc				1788
Leu Pro Arg Pro Ser *				
484	489			
caggagctgtatcactaccatgtttctggcacaattccagcacaattatgacaattcaga				1848
gaagcaagtc aaaggactgg gcacctgcctctgacagaca ccagaccagg tccagggcct				1908
cctccacagcctcagctggg gctctcagca ccaaagaacg agggggccag gtcttgg				1968
caccccgaaa gcccactgccc aggggtatgg tggccagctc agggcttcgtcgtact				2028
gtcgccccaga ccaggtgcca ttcatgacta atcaggagca gccccctcac ccaggcacct				2088
gtctgccagg agggccacgtgtgtcctgccc acccaggggg agctgtattt tggcagcacc				2148
ccacgcttgc tgcccgaggg cctcttgggg cacctaagac agcaccctctcagggag				2208

accatggtgg ccccgccgc acccccccac cctggtgcca ccactgcaac ttttgttac	2268
acaggcatcc catctccatc acagataaaa tcttaggaga taaacacatt caaaaaggaa	2328
tgagataaaa agaataaggc aataaatgtt gattggaacc tctcaagatt acagaaaata	2388
atgagaatga aattttaaaa aaaaaaaaaa	2416

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<400> 567

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Met Pro Tyr Ser Leu Asn Leu Ala Ile Arg Asp Thr Phe Val Asn Ala	
1 5 10	

tct cgg acc ctg tac agc agc ccc aga gtc cta agc aac aac agt	96
Ser Arg Thr Leu Tyr Ser Ser Pro Arg Val Leu Ser Asn Asn Ser	
17 22 27 32	

gac gcc aac ttg gag ctc atc aac acc tgg gtg gcc aag aac acc aac	144
Asp Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn Thr Asn	
33 38 43 48	

aac aag atc agc cgg ctg cta gac agt ctg ccc tcc gat acc cgc ctt	192
Asn Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr Arg Leu	
49 54 59 64	

gtc ctc ctc aat gct atc tac ctg agt gcc aag tgg aag aca aca ttt	240
Val Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr Thr Phe	
65 70 75 80	

gat ccc aag aaa acc aga atg gaa ccc ttt cac ttc aaa aac tca gtt	288
Asp Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn Ser Val	
81 86 91 96	

ata aaa gtg ccc atg atg aat agc aag aag tac cct gtg gcc cat ttc	336
Ile Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala His Phe	
97 102 107 112	

att gac caa act ttg aaa gcc aag ttg agt cgt ggg gac agc ttg aag	384
Ile Asp Gln Thr Leu Lys Ala Lys Leu Ser Arg Gly Asp Ser Leu Lys	
113 118 123 128	

gag cca acc tca att gca gag agc agc cgt cac ccc agc tac cgc tca	432
Glu Pro Thr Ser Ile Ala Glu Ser Ser Arg His Pro Ser Tyr Arg Ser	
129 134 139 144	

gag ccc agc ttg gaa cca gag agc ttc cgt tct cct acc ttt ggc aaa Glu Pro Ser Leu Glu Pro Glu Ser Phe Arg Ser Pro Thr Phe Gly Lys 145 150 155 160	480
agt ttt cac ttc gat cca cta tcc agt ggc tca cgc tcc tcc agc ctc Ser Phe His Phe Asp Pro Leu Ser Ser Gly Ser Arg Ser Ser Ser Leu 161 166 171 176	528
aag tca gcc cag ggc aca ggc ttt gag ctg ggc cag ttg caa tcc att Lys Ser Ala Gln Gly Thr Gly Phe Glu Leu Gly Gln Leu Gln Ser Ile 177 182 187 192	576
cgt tca gag ggc acc acc tcc acc tcc tat aag agc ctg gcc aac cag Arg Ser Glu Gly Thr Ser Thr Ser Tyr Lys Ser Leu Ala Asn Gln 193 198 203 208	624
aca cgc aat gga agc cta tct tat gac agc ttg ctc aca cct tca gac Thr Arg Asn Gly Ser Leu Ser Tyr Asp Ser Leu Leu Thr Pro Ser Asp 209 214 219 224	672
agc cct gat ttt gag tca gtg cag gca ggg cct gag cca gac cca cct Ser Pro Asp Phe Glu Ser Val Gln Ala Gly Pro Glu Pro Asp Pro Pro 225 230 235 240	720
tta ggc tat acc tct ccc ttc ctg tca gcc agg ctg gcc cag caa cgg Leu Gly Tyr Thr Ser Pro Phe Leu Ser Ala Arg Leu Ala Gln Gln Arg 241 246 251 256	768
gaa gct gag agg cac cca cgt ttg gtg cca act ggc cca aca cac cga Glu Ala Glu Arg His Pro Arg Leu Val Pro Thr Gly Pro Thr His Arg 257 262 267 272	816
gag ccc tca cca gtc cgt tac gac aat ctg tcg cgc cac att gtg gcc Glu Pro Ser Pro Val Arg Tyr Asp Asn Leu Ser Arg His Ile Val Ala 273 278 283 288	864
tct ctc cag gaa cga gag aag ttg ctg cgc cag tca ccc cca ctc ccg Ser Leu Gln Glu Arg Glu Lys Leu Leu Arg Gln Ser Pro Pro Leu Pro 289 294 299 304	912
ggc cgt gag gaa cca ggc ttg ggg gac tca ggc att cag tca aca Gly Arg Glu Glu Glu Pro Gly Leu Gly Asp Ser Gly Ile Gln Ser Thr 305 310 315 320	960
cca ggc tcg ggc cat gcc cct cgt act agt tcc tcc tca gat gat tca Pro Gly Ser Gly His Ala Pro Arg Thr Ser Ser Ser Asp Asp Ser 321 326 331 336	1008
aag aga tca cct ttg ggc aag act cca ctg gga cgc cca gct gtc ccc Lys Arg Ser Pro Leu Gly Lys Thr Pro Leu Gly Arg Pro Ala Val Pro 337 342 347 352	1056
cgt ttt ggc aag cca gat ggg cta agg ggc cgg gga gta ggg tcc cct Arg Phe Gly Lys Pro Asp Gly Leu Arg Gly Arg Gly Val Gly Ser Pro 353 358 363 368	1104
gaa cca ggc cca aca gcc cca tac ctg ggc cga tcg atg tct tac agc	1152

agagggata cctgggttct aacctctaaa tagggagat cccagcctcc acaaagaggc	2473
ccttttattt tttattctga ttagccattt taaaccaacg aggaataaaa agaaatcctg	2533
atctaaaaaa aaaaaa	2549

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 <213> Homo sapiens

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 <222> (304)..(1992)

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tcggatagtg gctggtaaaa acagaaaaac atcaaacaag ccatcaaatc tctgaaaaaa	120
tatagtgaca aatcagcaga aaagagtcct tttccagaag agaaaagtca cattatagac	180
aaagaagaag atataggtaa acgcagtctt tttcattaca caagttctat aaccacaaaa	240
tttggagact cattctactt tttatcaaattt catattaattt catatttcaa acgtaaggaa	300
aaa atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa tca gaa	348
Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu	
1 5 10	
ctt gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca gat cct	396
Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro	
16 21 26 31	
ggc atc ctg gct tat aag cca ggc tca gaa tct gta cat acg gtg gac	444
Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp	
32 37 42 47	
aag cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt tca act	492
Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr	
48 53 58 63	
aaa caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt gta caa	540
Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln	
64 69 74 79	
gct tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta aag tat	588
Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr	
80 85 90 95	
gat tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa act gat	636
Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Pro Ala Lys Thr Asp	
96 101 106 111	

cag gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt tta tct Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser 112 117 122 127	684
ctt cag cga gaa aag att atc gca agg gtg agt att gat aac agg acc Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr 128 133 138 143	732
cgg gca tta gtt cag gca tta aga aga aca act gac cca aag ctc tgc Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys 144 149 154 159	780
att act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt cct gaa Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu 160 165 170 175	828
gga aaa gga gtg gct gtc aag gaa aga att att cca tat tta tta cga Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg 176 181 186 191	876
ctg aga caa att aag gat gaa act ctt cag gct gca gtt aga gaa att Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile 192 197 202 207	924
ttg gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga atc cga Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg 208 213 218 223	972
att ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct ctc cag Ile Leu Ser Ile Asp Gly Gly Thr Arg Gly Val Val Ala Leu Gln 224 229 234 239	1020
acc cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat cag ctc Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu 240 245 250 255	1068
ttt gat tac att tgt ggt gta agc aca ggt gcc ata tta gct ttc atg Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met 256 261 266 271	1116
ttg ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt tat cga Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg 272 277 282 287	1164
aaa tta gga tca gat gta ttt tca ¹ caa aat gtc att gtt gga aca gta Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val 288 293 298 303	1212
aaa atg agt tgg agc cat gca ttt tat gac agt caa aca tgg gaa aac Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn 304 309 314 319	1260
att ctt aag gat agg atg gga tct gca ctg atg att gaa aca gca aga Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg 320 325 330 335	1308
aac ccc aca tgt cct aag gta gct gct gta agt acc ata gta aat aga	1356

Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg			
336	341	346	351
ggg ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat ttt cct			1404
Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro			
352	357	362	367
gga atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg tgg cag			1452
Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln			
368	373	378	383
gcc att aga gcc tca tct gct gct cca ggc tac ttt gca gaa tat gca			1500
Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala			
384	389	394	399
ttg gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat aac cct			1548
Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro			
400	405	410	415
tcg gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat gtg ccg			1596
Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro			
416	421	426	431
tta gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt gat gtg			1644
Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val			
432	437	442	447
aga aac acg gta aca tac aca agc ttg aaa act aaa ctt tct aat gtt			1692
Arg Asn Thr Val Thr Ser Leu Lys Thr Lys Leu Ser Asn Val			
448	453	458	463
atc aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt gat ggc			1740
Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly			
464	469	474	479
ctg tta cct cct gac acc tat ttt aga ttc aat cct gta atg tgt gaa			1788
Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu			
480	485	490	495
aac ata cct cta gat gaa agt cga aat gaa aag ctg gat cag ctg cag			1836
Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln			
496	501	506	511
ttg gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg aaa aaa			1884
Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys			
512	517	522	527
gtt gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa att aat			1932
Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn			
528	533	538	543
gat tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca ttc ttt			1980
Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe			
544	549	554	559
tca aaa ttg tga tga gtatatgctt atgttctcat aaatgaaggt ctgttttagaa			2035
Ser Lys Leu *			

gatcaaccac attcaataag gaattgtggg gttcgacatg agttaacttt gaaatacgta	2095
tgaattctgg agaattcctga aaaagacggt gcttcaacca gcttgcatac cacagagaat	2155
attcttggtt acagaattca tatggaaact aggctttaa gatgttaata attagctaag	2215
cttttagtaac ccttactgtg ctagtagatt ttagtagata ttgggtttat attgtttgat	2275
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Met Gly Glu Ser	
1	
agt gaa gac ata gac caa atg ttc agc act ttg ctg gga gag atg gat	162
Ser Glu Asp Ile Asp Gln Met Phe Ser Thr Leu Leu Gly Glu Met Asp	
5 10 15 20	
ctt ctg act cag tta gga gtt gac act ctc cct cct gac cct	210
Leu Leu Thr Gln Ser Leu Gly Val Asp Thr Leu Pro Pro Pro Asp Pro	
21 26 31 36	
aat cca ccc aga gct gaa ttt aac tac agt gtg ggg ttt aaa gat tta	258
Asn Pro Pro Arg Ala Glu Phe Asn Tyr Ser Val Gly Phe Lys Asp Leu	
37 42 47 52	
aat gag tcc tta aat gca ctg gaa gac caa gat tta gat gct ctc atg	306
Asn Glu Ser Leu Asn Ala Leu Glu Asp Gln Asp Leu Asp Ala Leu Met	
53 58 63 68	
gca gat ctg gta gca gac ata agt gag gct gag cag agg aca atc cag	354
Ala Asp Leu Val Ala Asp Ile Ser Glu Ala Glu Gln Arg Thr Ile Gln	
69 74 79 84	
gca cag aaa gag tcc ttg cag aat caa cat cat tca gca tct cta caa	402
Ala Gln Lys Glu Ser Leu Gln Asn Gln His His Ser Ala Ser Leu Gln	
85 90 95 100	
gca tca att ttc agt ggt gca gcc tct ctt ggt tat gga aca aat gtt	450
Ala Ser Ile Phe Ser Gly Ala Ala Ser Leu Gly Tyr Gly Thr Asn Val	

101	106	111	116	
gct gcc act ggt atc agc caa tat gag gat gac tta cca cct cca cca				498
Ala Ala Thr Gly Ile Ser Gln Tyr Glu Asp Asp Leu Pro Pro Pro Pro				
117	122	127	132	
gcc gat cct gtg tta gac ctt cca ctg cca cca cct cct gaa cct				546
Ala Asp Pro Val Leu Asp Leu Pro Leu Pro Pro Pro Pro Glu Pro				
133	138	143	148	
ctc tct cag gaa gag gaa gaa gcc caa gaa aag gct gat aaa att aag				594
Leu Ser Gln Glu Glu Glu Ala Gln Ala Lys Ala Asp Lys Ile Lys				
149	154	159	164	
ctg gcg ctg gaa aaa ctg aag gag gcc aag gtt aag aag ctc gtc gtc				642
Leu Ala Leu Glu Lys Leu Lys Glu Ala Lys Val Lys Lys Leu Val Val				
165	170	175	180	
aag gtg cac atg aat gat aac agc aca aag tca ctg atg gtg gat gag				690
Lys Val His Met Asn Asp Asn Ser Thr Lys Ser Leu Met Val Asp Glu				
181	186	191	196	
cg ^g cag ctg gcc cga gat gtt ctg gac aac ctt ttc gag aaa act cat				738
Arg Gln Leu Ala Arg Asp Val Leu Asp Asn Leu Phe Glu Lys Thr His				
197	202	207	212	
tgt gac tgc aat gta gac tgg tgt ctt tat gaa atc tac ccg gaa cta				786
Cys Asp Cys Asn Val Asp Trp Cys Leu Tyr Glu Ile Tyr Pro Glu Leu				
213	218	223	228	
caa att gag agg ttt ttt gaa gac cat gaa aat gtt gtt gaa gtc tta				834
Gln Ile Glu Arg Phe Phe Glu Asp His Glu Asn Val Val Glu Val Leu				
229	234	239	244	
tca gac tgg aca aga gac aca gaa aat aaa ata cta ttt ttg gag aaa				882
Ser Asp Trp Thr Arg Asp Thr Glu Asn Lys Ile Leu Phe Leu Glu Lys				
245	250	255	260	
gag gag aaa tat gct gta ttt aaa aac ccc cag aat ttc tac ttg gat				930
Glu Glu Lys Tyr Ala Val Phe Lys Asn Pro Gln Asn Phe Tyr Leu Asp				
261	266	271	276	
aac aga gga aaa aaa gaa agc aag gaa act aat gag aaa atg aat gct				978
Asn Arg Gly Lys Lys Glu Ser Lys Glu Thr Asn Glu Lys Met Asn Ala				
277	282	287	292	
aag aac aag gaa tcc tta ctt gag gta agg tta att ttg cag agt gga				1026
Lys Asn Lys Glu Ser Leu Leu Glu Val Arg Leu Ile Leu Gln Ser Gly				
293	298	303	308	
aga aaa gag aag gac gtt tgc tct att ttt aag tca ttt gct tcc gag				1074
Arg Lys Glu Lys Asp Val Cys Ser Ile Phe Lys Ser Phe Ala Ser Glu				
309	314	319	324	
/ aac aat gga aaa atc taa agacat acactgaaat tttaagttgg ggtgttaaaa				1128
Asn Asn Gly Lys Ile *				
325	330			

tcaaattatt tctaaattat agctatTTAG ataattcaac tgTTTTCTT ttttgagtca	1188
tttGTTacaa catgtggctt tagataaaatg aagctggatt tgtaattctt gactttaaa	1248
aaactctagc attccaagtt tccattactt a	1279

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<400> 570

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cagcggctgc tggagccgcg acagtacatg ctgctgctgc ccgagcacgt gctggtcaag	120
atcttcagct tcctgcccac gcgcgcgctg gccggccctca agtgcacactg ccaccacttc	180
aagggcatca tcgaggcggtt tggcgtgcgg gccacagact cgcgctggag ccgagaccgg	240
ctctaccgcg atg atc cgt gca aac agt gcc gca aga gat acg aga agg	289
Met Ile Arg Ala Asn Ser Ala Ala Arg Asp Thr Arg Arg	
1 5 10	

gcg acg tgt cgc tct gcc gct ggc acc cca agc cct acc acc atg acc	337
Ala Thr Cys Arg Ser Ala Ala Gly Thr Pro Ser Pro Thr Thr Met Thr	
14 19 24 29	

tgc ctt acg gac gtt cct act gga tgt gct gcc gtc gag ccg acc gcg	385
Cys Leu Thr Asp Val Pro Thr Gly Cys Ala Ala Val Glu Pro Thr Ala	
30 35 40 45	

aga ctc ccg gct gcc gcc tgg gcc tcc acg ata aca act ggg tgc tgc	433
Arg Leu Pro Ala Ala Trp Ala Ser Thr Ile Thr Thr Gly Cys Cys	
46 51 56 61	

cct gca atg ggc cag gcg ggg gcc ggg ccg gcc ggg agg aag gga agt	481
Pro Ala Met Gly Gln Ala Gly Ala Gly Pro Ala Gly Arg Lys Gly Ser	
62 67 72 77	

gaa gcc ggg gga ggg ccg ggg aga gcc cac cac gcc cac ccc tcc cct	529
Glu Ala Gly Gly Pro Gly Arg Ala His His Ala His Pro Ser Pro	
78 83 88 93	

ctc ccc ccg gag ccg agg gtc cgG act ggg ccg cct gcc cat tcc cct	577
Leu Pro Arg Glu Pro Arg Val Arg Thr Gly Pro Pro Ala His Ser Pro	
94 99 104 109	

act cca ggc agc att gat ccc tca ccg gaa ctg agc tgg ggt tca gca	625
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Thr Pro Gly Ser Ile Asp Pro Ser Pro Glu Leu Ser Trp Gly Ser Ala			
110	115	120	125
ggg gtg acc cag gaa agc cct ctg ctt gat cct gtt gat ttt cta ctc			673
Gly Val Thr Gln Glu Ser Pro Leu Leu Asp Pro Val Asp Phe Leu Leu			
126	131	136	141
ttc aga acc agg gcc gtg gac cct ctg aga agg gtg ttt ttt ttt			721
Phe Arg Thr Arg Ala Val Asp Pro Leu Arg Arg Val Phe Phe Phe Phe			
142	147	152	157
tat cag cat ctc act ttc ttc tcc att cag ccc caa ccc cct ccc tgc			769
Tyr Gln His Leu Thr Phe Phe Ser Ile Gln Pro Gln Pro Pro Pro Cys			
158	163	168	173
cat gct ttc cac ccc aag gac cca cca gca ggg agc aga cgg cag cta			817
His Ala Phe His Pro Lys Asp Pro Pro Ala Gly Ser Arg Arg Gln Leu			
174	179	184	189
att ttg gta cca ctt aag ggt ccc ccc att ctg gcc ccc atc ctc tcc			865
Ile Leu Val Pro Leu Lys Gly Pro Pro Ile Leu Ala Pro Ile Leu Ser			
190	195	200	205
ctc acc cca att ctt tct cgc tgg agc tgt tat ttc cca aga agc cgc			913
Leu Thr Pro Ile Leu Ser Arg Trp Ser Cys Tyr Phe Pro Arg Ser Arg			
206	211	216	221
atc gcc caa ggt tgg cac ctc tcc taa cctgc cacacgacag ctctcacctc			965
Ile Ala Gln Gly Trp His Leu Ser *			
222	227		
tcttaggaatt gggggctgtc aggtcacagg tggatctgg cattttttta tgacagtcca			1025
tttcttagatg gtttgcctat taaagaagtg gggggaaat actgtttct ccttaacctc			1085
aagctaccag tctctcctct tccgcgtaga ggaagagggg ggcagacaaa aaaaaagctg			1145
aagtataaaa accctcctcc tcccgttatt attaagcta ctgccatcaa ccccacccccc			1205
ataaagctgt gaagcccttt gcctcgctt tgacagcgtg gggggcccccc gtgggcaggg			1265
acttcggatt tgcatttctg gttttttt cttccactc tgggtctcg ttcaggcatt			1325
ggggctcct caccctcagcc acatgtttct ttaagaatcc tttggtaac caggaccttg			1385
attttcagg cattttggtc tgggttatt ttgtttgttc tctctgttt ttgtttctt			1445
tttttctt ccatcgtggt tctggaaagct tctagcgtgt ggcatctgac caatttgaa			1505
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<210> 571
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1650)

<400> 571

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1		5				10											
ctg	cac	cg	cct	ttc	tac	ccg	gct	gtc	gag	ggc	acc	ctg	tgc	ctg	acg	96	
Leu	His	Arg	Pro	Phe	Tyr	Pro	Ala	Val	Glu	Gly	Thr	Leu	Cys	Leu	Thr		
17				22				27				32					
ggc	cac	cac	ttg	atc	ctg	tcc	ccg	cag	gac	aat	acg	gag	gag	ctg	144		
Gly	His	His	Leu	Ile	Leu	Ser	Ser	Arg	Gln	Asp	Asn	Thr	Glu	Glu	Leu		
33				38				43				48					
tgg	ctc	ctc	cat	tca	aac	atc	gac	gcc	atc	gac	aag	cga	ttt	gta	gga	192	
Trp	Leu	Leu	His	Ser	Asn	Ile	Asp	Ala	Ile	Asp	Lys	Arg	Phe	Val	Gly		
49					54				59			64					
tca	ctg	ggt	acc	atc	atc	ata	aaa	tgt	aaa	gat	ttt	cga	att	att	cag	240	
Ser	Leu	Gly	Thr	Ile	Ile	Lys	Cys	Lys	Asp	Phe	Arg	Ile	Ile	Gln			
65				70				75			80						
ttg	gat	att	cct	gga	atg	gag	gaa	tgc	ttg	aat	ata	gcc	agt	tcc	att	288	
Leu	Asp	Ile	Pro	Gly	Met	Glu	Glu	Cys	Leu	Asn	Ile	Ala	Ser	Ser	Ile		
81					86				91			96					
gag	gca	ttg	tct	act	ctg	gac	tcc	atc	act	ctg	atg	tac	cct	ttc	ttt	336	
Glu	Ala	Leu	Ser	Thr	Leu	Asp	Ser	Ile	Thr	Leu	Met	Tyr	Pro	Phe	Phe		
97					102				107			112					
tac	cgt	cct	atg	ttt	gaa	gtg	ata	gaa	gat	ggc	tgg	cat	tcc	ttc	ctt	384	
Tyr	Arg	Pro	Met	Phe	Glu	Val	Ile	Glu	Asp	Gly	Trp	His	Ser	Phe	Leu		
113					118				123			128					
cct	gag	caa	gaa	ttt	gaa	ctc	tat	tct	tca	gct	acc	agt	gaa	tgg	agg	432	
Pro	Glu	Gln	Glu	Phe	Glu	Leu	Tyr	Ser	Ser	Ala	Thr	Ser	Glu	Trp	Arg		
129					134				139			144					
cta	agc	tat	gtc	aat	aag	gaa	ttt	gct	gtc	tgt	ccc	tct	tac	cca	cca	480	
Leu	Ser	Tyr	Val	Asn	Lys	Glu	Phe	Ala	Val	Cys	Pro	Ser	Tyr	Pro	Pro		
145					150				155			160					
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Ile	Val	Thr	Val	Pro	Lys	Ser	Ile	Asp	Asp	Glu	Ala	Leu	Arg	Lys	Val		
161					166				171			176					
gct	aca	ttt	cga	cat	gga	ggg	cgc	ttc	cca	gta	cta	agc	tat	tac	cac	576	
Ala	Thr	Phe	Arg	His	Gly	Gly	Arg	Phe	Pro	Val	Leu	Ser	Tyr	Tyr	His		
177					182				187			192					
aaa	aga	aat	ggg	atg	gta	att	atg	cga	agt	ggt	cag	cca	ctc	act	ggt	624	
Lys	Arg	Asn	Gly	Met	Val	Ile	Met	Arg	Ser	Gly	Gln	Pro	Leu	Thr	Gly		

193	198	203	208	
aca aac ggg agg agg tgc aag gag gac gag aag ctg ata aat gct acc				672
Thr Asn Gly Arg Arg Cys Lys Glu Asp Glu Lys Leu Ile Asn Ala Thr				
209	214	219	224	
ctc agg gct gga aag cgt ggc tac atc att gac acc cga tcc ctg aac				720
Leu Arg Ala Gly Lys Arg Gly Tyr Ile Ile Asp Thr Arg Ser Leu Asn				
225	230	235	240	
gtg gct cag caa act aga gcc aaa gga ggt ggc ttt gaa caa gaa gct				768
Val Ala Gln Gln Thr Arg Ala Lys Gly Gly Phe Glu Gln Glu Ala				
241	246	251	256	
cat tat cct cag tgg agg cga att cat aag tcc att gag agg tat cac				816
His Tyr Pro Gln Trp Arg Arg Ile His Lys Ser Ile Glu Arg Tyr His				
257	262	267	272	
att ctt cag gag agc tta atc aaa ctt gtg gaa gct tgt aat gac caa				864
Ile Leu Gln Glu Ser Leu Ile Lys Leu Val Glu Ala Cys Asn Asp Gln				
273	278	283	288	
aca cat aac atg gac cga tgg ctc agt aaa ttg gag gcc tct aac tgg				912
Thr His Asn Met Asp Arg Trp Leu Ser Lys Leu Glu Ala Ser Asn Trp				
289	294	299	304	
ctg act cac atc aaa gag att ctg aca acc gcc tgc cta gcg gct cag				960
Leu Thr His Ile Lys Glu Ile Leu Thr Thr Ala Cys Leu Ala Ala Gln				
305	310	315	320	
tgc atc gac agg gaa gga gca tca ata ttg att cac gga aca gaa gga				1008
Cys Ile Asp Arg Glu Gly Ala Ser Ile Leu Ile His Gly Thr Glu Gly				
321	326	331	336	
act gat tcc aca ctc cag gtg acc tcc ttg gcc cag atc atc tta gag				1056
Thr Asp Ser Thr Leu Gln Val Thr Ser Leu Ala Gln Ile Ile Leu Glu				
337	342	347	352	
cca aga agc agg acc att cgt ggt ttt gag gcc ctg att gaa aga gag				1104
Pro Arg Ser Arg Thr Ile Arg Gly Phe Glu Ala Leu Ile Glu Arg Glu				
353	358	363	368	
tgg ctg cag gct ggt cac cca ttc cag cag cgc tgt gca cag tca gcc				1152
Trp Leu Gln Ala Gly His Pro Phe Gln Gln Arg Cys Ala Gln Ser Ala				
369	374	379	384	
tac tgt aac acc aag cag aag tgg gag gct cct gta ttt ctt ctc ttc				1200
Tyr Cys Asn Thr Lys Gln Lys Trp Glu Ala Pro Val Phe Leu Leu Phe				
385	390	395	400	
ttg gac tgc gtg tgg cag atc ctt cgt cag ttt ccc tgt tct ttt gag				1248
Leu Asp Cys Val Trp Gln Ile Leu Arg Gln Phe Pro Cys Ser Phe Glu				
401	406	411	416	
ttt aat gag att ttc ctc atc atg ctc ttt gag cat gct tat gcc tca				1296
Phe Asn Glu Ile Phe Leu Ile Met Leu Phe Glu His Ala Tyr Ala Ser				
417	422	427	432	

cag ttt gga aca ttt ctg ggc aac aat gaa agt gaa aga tgt aag ttg Gln Phe Gly Thr Phe Leu Gly Asn Asn Glu Ser Glu Arg Cys Lys Leu 433 438 443 448	1344
aag cta cag cag aag acg atg tct ttg tgg tcc tgg gtt aat cag ccc Lys Leu Gln Gln Lys Thr Met Ser Leu Trp Ser Trp Val Asn Gln Pro 449 454 459 464	1392
agt gag ctg agt aaa ttc acc aat ccc ctc ttt gaa gcc aac aac ctt Ser Glu Leu Ser Lys Phe Thr Asn Pro Leu Phe Glu Ala Asn Asn Leu 465 470 475 480	1440
gtc atc tgg cct tca gtt gct ccg cag agt ctt cca ctg tgg gaa ggt Val Ile Trp Pro Ser Val Ala Pro Gln Ser Leu Pro Leu Trp Glu Gly 481 486 491 496	1488
att ttc cta cgt tgg aat aga tcc tct aag tat ttg gat gaa gca tat Ile Phe Leu Arg Trp Asn Arg Ser Ser Lys Tyr Leu Asp Glu Ala Tyr 497 502 507 512	1536
gaa gaa atg gtt aac atc att gaa tat aat aaa gaa tta caa gca aaa Glu Glu Met Val Asn Ile Ile Glu Tyr Asn Lys Glu Leu Gln Ala Lys 513 518 523 528	1584
gtc aat atc ctt cga agg cag ttg gca gaa ctg gaa aca gag gac ggg Val Asn Ile Leu Arg Arg Gln Leu Ala Glu Leu Glu Thr Glu Asp Gly 529 534 539 544	1632
atg cag gag agt ccc tga aaggtc tcctcgacc cttcgcaagg accttcttgg Met Gln Glu Ser Pro *545 550	1686
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<210> 572
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 <213> Homo sapiens

<220>
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 <222> (202)..(1212)

<220>
 <221> misc_feature
 <222> (1)..(2728)
 <223> n = a,t,c or g

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<400> 572

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gtgtcttgct cacatcgtaa atgactttct ctccgaaacg ctaaatattc tttcccgca	180
gagctcatat ccttattttc c atg aca gat ctt aac gac aat ata tgc aaa	231
Met Thr Asp Leu Asn Asp Asn Ile Cys Lys	
1 5	
aga tat ata aag atg ata act aat ata gtt ata ctg agc ctg atc att	279
Arg Tyr Ile Lys Met Ile Thr Asn Ile Val Ile Leu Ser Leu Ile Ile	
11 16 21 26	
tgc att tcg tta gct ttc tgg att ata tca atg act gca agc acc tat	327
Cys Ile Ser Leu Ala Phe Trp Ile Ser Met Thr Ala Ser Thr Tyr	
27 32 37 42	
tat ggt aac tta cga cct att tct ccg tgg cgt tgg ctg ttt tct gtt	375
Tyr Gly Asn Leu Arg Pro Ile Ser Pro Trp Arg Trp Leu Phe Ser Val	
43 48 53 58	
gtt gtt cct gtt ctg atc gtc tct aat ggc ctt aaa aag aaa agt cta	423
Val Val Pro Val Leu Ile Val Ser Asn Gly Leu Lys Lys Ser Leu	
59 64 69 74	
gat cac agt ggg gct cta gga ggg cta gtc gtt gga ttt atc cta acc	471
Asp His Ser Gly Ala Leu Gly Leu Val Val Gly Phe Ile Leu Thr	
75 80 85 90	
att gca aat ttc agc ttt ttt acc tct ttg ctg atg ttt ttc ttg tct	519
Ile Ala Asn Phe Ser Phe Phe Thr Ser Leu Leu Met Phe Phe Leu Ser	
91 96 101 106	
tct tcg aaa ctc act aaa tgg aag gga gaa gtg aag aag cgt cta gat	567
Ser Ser Lys Leu Thr Lys Trp Lys Gly Glu Val Lys Lys Arg Leu Asp	
107 112 117 122	
tca gaa tat aag gaa ggt ggg caa agg aat tgg gtt cag gtg ttc tgt	615
Ser Glu Tyr Lys Glu Gly Gln Arg Asn Trp Val Gln Val Phe Cys	
123 128 133 138	
aat gga gct gta ccc aca gaa ctg gcc ctg tac atg ata gaa aat	663
Asn Gly Ala Val Pro Thr Glu Leu Ala Leu Tyr Met Ile Glu Asn	
139 144 149 154	
ggc ccc ggg gaa atc cca gtc gat ttt tcc aag cag tac tcc gct tcc	711
Gly Pro Gly Glu Ile Pro Val Asp Phe Ser Lys Gln Tyr Ser Ala Ser	
155 160 165 170	
tgg atg tgt ttg tct ctc ttg gct gca ctg gcc tgc tct gct gga gac	759
Trp Met Cys Leu Ser Leu Ala Ala Leu Ala Cys Ser Ala Gly Asp	
171 176 181 186	
aca tgg gct tca gaa gtt ggc cca gtt ctg agt aaa agt tct cca aga	807
Thr Trp Ala Ser Glu Val Gly Pro Val Leu Ser Lys Ser Ser Pro Arg	
187 192 197 202	
ctg ata aca acc tgg gag aaa gtt cca gtt ggt acc aat gga gga gtt	855
Leu Ile Thr Thr Trp Glu Lys Val Pro Val Gly Thr Asn Gly Gly Val	

203	208	213	218			
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Val	Val	Gly	Leu			
219	224	229	234			
235	240	245	250	951		
251	256	261	266	999		
267	272	277	282	1047		
283	288	293	298	1095		
299	304	309	314	1143		
315	320	325	330	1191		
331	336			1244		
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gcggaaatgc	cagttcctcc	tgtattccat	tgagatggga	tttcacattt	tcctctcatc	1364
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gaatgtatga	aaaaaatcat	tttaactaaa	agcaaaaagaa	ttttatctta	tatctaaaaaa	1904
atataataact	tactatatgt	ttcagttgct	ctctgaacaa	aaattatctt	caatttaata	1964

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aggattttag	aatacaccac	caccagagtg	gataatgctt	agaattctt	attgggtggcc	2384
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cattggaagc	accagggcat	gtttgctttt	tttgtttatg	tgTTTgtttt	ttgagacaga	2564
gtctcacact	gtgttcccag	ccactcgga	ggctgaggca	ggagaatcgc	tggaacctgg	2624
gatgtggagg	ttgcagtgag	ccaagattgc	accactgtac	tccagcctgg	gcaacagagg	2684
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<220>
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<400> 573

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gtaaaagaagc	agctcttgaa	gctcaccttg	tccctgtctt	gcactctctc	tggccttgaa	180
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atTTTccaaa	tggttgcagt	tctctttgtt	ggtcaagttg	tggacaacac	cctgttcaag	300
ctacacatag	aggagccgtg	agcaactctc	tgg atg	ctg tgt atc	cta aag ttg	354
			Met	Leu	Cys Ile	Leu Lys Leu
			1		5	

gct tcc cag atg cca ctg gag aac acc acg gtt cag cag atg gtt ttt	402		
Ala Ser Gln Met Pro Leu Glu Asn Thr Thr Val Gln Gln Met Val Phe			
8	13	18	23

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cag aag agt aac ttc tta cag aac ttc ctc tct cta gca ttg cca aaa Gln Lys Ser Asn Phe Leu Gln Asn Phe Leu Ser Leu Ala Leu Pro Lys 40 45 50 55	498
gga gga aat aaa cat cta agt aat ctg act att ctt tgg ttg aag tta Gly Gly Asn Lys His Leu Ser Asn Leu Thr Ile Leu Trp Leu Lys Leu 56 61 66 71	546
ctc ctg aat ata tca tct gga gaa gat ggg caa caa atg att ctg agg Leu Leu Asn Ile Ser Ser Gly Glu Asp Gly Gln Gln Met Ile Leu Arg 72 77 82 87	594
ctt gat ggc tgt cta gac tta cta aca gag atg agc aaa tac aag cac Leu Asp Gly Cys Leu Asp Leu Leu Thr Glu Met Ser Lys Tyr Lys His 88 93 98 103	642
aag agc agc cct tta ttg cct ctt atc ttt cat aat gtt tgc ttc Lys Ser Ser Pro Leu Leu Pro Leu Leu Ile Phe His Asn Val Cys Phe 104 109 114 119	690
agt cct gca aat aaa ccc aag atc ctg gct aat gaa aaa gtc att act Ser Pro Ala Asn Lys Pro Lys Ile Leu Ala Asn Glu Lys Val Ile Thr 120 125 130 135	738
gtg ctt gct gcc tgt ctg gaa agt gag aat caa aat gct cag agg att Val Leu Ala Ala Cys Leu Glu Ser Glu Asn Gln Asn Ala Gln Arg Ile 136 141 146 151	786
gga gca gct gcc ctt tgg gct ctg att tac aat tat cag aag gca aaa Gly Ala Ala Ala Leu Trp Ala Leu Ile Tyr Asn Tyr Gln Lys Ala Lys 152 157 162 167	834
aca gct ttg aaa agc cca tca gta aaa aga aga gtg gat gaa gca tac Thr Ala Leu Lys Ser Pro Ser Val Lys Arg Arg Val Asp Glu Ala Tyr 168 173 178 183	882
tcc tta gca aag aaa act cct taa ttcttcctga gtgccatggg atgctacacc Ser Leu Ala Lys Lys Thr Pro *	936
184 189	
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1056	
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1270	

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<220>
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<220>
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<400> 574

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acaaaatagg	aattccaagg	aactgggcct	agttcccctc	acagatgaca	ccagccacgc	180
caggcctcca	gggccaggga	gggcactgct	ggagtgtgac	cacctgagga	gtggggtgcc	240
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					Met Pro Pro Pro	
					1	
cgg aag cac act	ttg ctg gcc	aat aat ggg	ttt gca	att tct gct	gca	404
Arg Lys His	Thr Leu Leu	Ala Asn Asn	Gly Phe	Ala Ile Ser	Ala Ala	
5	10	15	20			
ttg ctg atg gcc	tgc tcg ctc	cag gca gga	gcc ttt gaa	atg ctc atc		452
Leu Leu Met	Ala Cys Ser	Leu Gln Ala	Gly Ala Phe	Glu Met Leu	Ile	
21	26	31	36			
gtg gga cgc ttc	atc atg ggc	ata gat gga	ggc gtc	gcc ctc	agt gtg	500
Val Gly Arg	Phe Ile Met	Gly Ile Asp	Gly Gly Val	Ala Leu	Ser Val	
37	42	47	52			
ctc ccc atg tac	ttt agt gag	atc tca ccc	aag gag	atc cgt ggc	tct	548
Leu Pro Met	Tyr Leu Ser	Glu Ile Ser	Pro Lys	Glu Ile	Arg Gly Ser	
53	58	63	68			
ctg ggg cag gtg	act gcc atc	ttt atc tgc	att ggc	gtg ttc	act ggg	596
Leu Gly Gln	Val Thr Ala	Ile Phe Ile	Cys Ile	Gly Val Phe	Thr Gly	
69	74	79	84			
cag ctt ctg ggc	ctg ccc gag	ctg gga aag	gag agt	acc tgg cca		644
Gln Leu Leu	Gly Leu Pro	Glu Leu Leu	Gly Lys	Glu Ser Thr	Trp Pro	
/85	90	95	100			
tac ctg ttt gga	gtg att gtc	cct gcc gtt	gtc cag	ctg ctg	agc	692

Tyr	Leu	Phe	Gly	Val	Ile	Val	Val	Pro	Ala	Val	Val	Gln	Leu	Leu	Ser	
101																116
ctt	ccc	ttt	ctc	ccg	gac	agc	cca	cgc	tac	ctg	ctc	ttg	gag	aag	cac	740
Leu	Pro	Phe	Leu	Pro	Asp	Ser	Pro	Arg	Tyr	Leu	Leu	Leu	Glu	Lys	His	
117																132
122										127						
aac	gag	gca	aga	gct	gtg	aaa	gcc	ttc	caa	acg	ttc	ttg	ggt	aaa	gca	788
Asn	Glu	Ala	Arg	Ala	Val	Lys	Ala	Phe	Gln	Thr	Phe	Leu	Gly	Lys	Ala	
133																148
138										143						
cac	gtt	tcc	caa	gag	gta	gag	gag	gtc	ctg	gct	gag	agc	cgc	gtg	cag	836
His	Val	Ser	Gln	Glu	Val	Glu	Glu	Val	Leu	Ala	Glu	Ser	Arg	Val	Gln	
149										159						164
154																
agg	agc	atc	cgc	ctg	gtg	tcc	gtg	ctg	gag	ctg	ctg	aga	gct	ccc	tac	884
Arg	Ser	Ile	Arg	Leu	Val	Ser	Val	Leu	Glu	Leu	Leu	Arg	Ala	Pro	Tyr	
165										175						180
170																
gtc	cgc	tgg	cag	gtg	gtc	acc	gtg	att	gtc	acc	atg	gcc	tgc	tac	cag	932
Val	Arg	Trp	Gln	Val	Val	Thr	Val	Ile	Val	Thr	Met	Ala	Cys	Tyr	Gln	
181										191						196
186																
ctc	tgt	ggc	ctc	aat	gca	att	tgg	ttc	tat	acc	aac	agc	atc	ttt	gga	980
Leu	Cys	Gly	Leu	Asn	Ala	Ile	Trp	Phe	Tyr	Thr	Asn	Ser	Ile	Phe	Gly	
197										207						212
202																
aaa	gct	ggg	atc	cct	ccg	gca	aag	atc	cca	tac	gtc	acc	ttg	agt	aca	1028
Lys	Ala	Gly	Ile	Pro	Pro	Ala	Lys	Ile	Pro	Tyr	Val	Thr	Leu	Ser	Thr	
213										223						228
218																
ggg	ggc	atc	gag	act	ttg	gct	gcc	gtc	ttc	tct	ggt	ttg	gtc	att	gag	1076
Gly	Gly	Ile	Glu	Thr	Leu	Ala	Ala	Val	Phe	Ser	Gly	Leu	Val	Ile	Glu	
229										239						244
234																
cac	ctg	gga	cgg	aga	ccc	ctc	ctc	att	ggt	ggc	ttt	ggg	ctc	atg	ggc	1124
His	Leu	Gly	Arg	Arg	Pro	Leu	Leu	Ile	Gly	Gly	Phe	Gly	Leu	Met	Gly	
245										255						260
250																
ctc	ttc	ttt	ggg	acc	ctc	acc	atc	acg	ctg	acc	ctg	cag	gac	cac	gcc	1172
Leu	Phe	Phe	Gly	Thr	Leu	Thr	Ile	Thr	Leu	Thr	Leu	Gln	Asp	His	Ala	
261										271						276
266																
ccc	tgg	gtc	ccc	tac	ctg	agt	atc	gtg	ggc	att	ctg	gcc	atc	atc	gcc	1220
Pro	Trp	Val	Pro	Tyr	Leu	Ser	Ile	Val	Gly	Ile	Leu	Ala	Ile	Ile	Ala	
277										287						292
282																
tct	ttc	tgc	agt	ggg	cca	ggt	ggc	atc	ccg	ttc	atc	ttg	act	ggt	gag	1268
Ser	Phe	Cys	Ser	Gly	Pro	Gly	Gly	Ile	Pro	Phe	Ile	Leu	Thr	Gly	Glu	
293										303						308
298																
ttc	ttc	cag	caa	tct	cag	ccg	ccg	gct	gcc	ttc	atc	att	gca	ggc	acc	1316
Phe	Phe	Gln	Gln	Ser	Gln	Arg	Pro	Ala	Ala	Phe	Ile	Ile	Ala	Gly	Thr	
309										319						324
314																
gtc	aac	tgg	ctc	tcc	aac	ttt	gct	gtt	ggg	ctc	ctc	ttc	cca	ttc	att	1364
Val	Asn	Trp	Leu	Ser	Asn	Phe	Ala	Val	Gly	Leu	Leu	Phe	Pro	Phe	Ile	
Asn	Trp	Leu	Ser	Asn	Phe	Ala	Val	Gly	Leu	Leu	Phe	Pro	Phe	Ile		
1364																

325	330	335	340	
cag aaa agt ctg gac acc tac tgt ttc cta gtc ttt gct aca att tgt Gln Lys Ser Leu Asp Thr Tyr Cys Phe Leu Val Phe Ala Thr Ile Cys 341	346	351	356	1412
atc aca ggt gct atc tac ctg tat ttt gtg ctg cct gag acc aaa aac Ile Thr Gly Ala Ile Tyr Leu Tyr Phe Val Leu Pro Glu Thr Lys Asn 357	362	367	372	1460
aga acc tat gca gaa atc agc cag gca ttt tcc aaa agg aac aaa gca Arg Thr Tyr Ala Glu Ile Ser Gln Ala Phe Ser Lys Arg Asn Lys Ala 373	378	383	388	1508
tac cca cca gaa gag aaa atc gac tca gct gtc act gat ggt aag ata Tyr Pro Pro Glu Glu Lys Ile Asp Ser Ala Val Thr Asp Gly Lys Ile 389	394	399	404	1556
aat gga agg cct taa caagttcct cctccacgtt ggacaattat gtcaaaaaca Asn Gly Arg Pro *	405			1611
ggattgtcta catggatgat ctcactttc agggaaactta aaatttaccc attattggga				1671
agcttaaatg aattgaagct atgcaagtct tttatattat taaatattta aaagtaaacc				1731
tgtactaatc taacattgca actgtgttag cattattcac aactgaatct cccaaaccct				1791
tctggaagct gcaaggaatc actctatgtt tcagtagacc cagcgttctt ctatatagg				1851
agatgacctg cttttcat gactcaaccc atgattcaa aatgaaattt gggaaatagt				1911
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gatcacagac tgaggttcta gtcccagctt taccacaagc agccttgacc tgccctcaac				2031
ctgggtccca gtgcctcaat gaccctaggc ttccatccct gatataaggct ttcagaagtc				2091
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gttcaccatc actcaaagtgc ctcaaggaa gactgggtga ttactcatct tgactgttgc				2631
taagaaaatc tttgtcaact ttggaggaag gtgtttggaa tagatatgtt gaggggctct				2691

tctaactctt acatgctaaa gttgttgag taagatctac ttacagcctg ccatcgtaat	2751
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cttccccagtc ccacgcgttt actcgatgaa ggcagcctcc caccgggctc ctggccccgc	180
ccgagccccca cccccctgctc cttccggcc cggactgggt cccatcgccc cacctccgggt	240
cgctggacgt gctctcgctg agctccgcct ttctgttgg ttagtattgg gatggggcct	295
atg Met	
Met 1	

atg gct gcg gtg ccg ccg ggc ctg gag ccg tgg aac cgt gtg aga atc	343
Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg Ile	
2 7 12 17	

cct aag gcg ggg aac cgc agc gca gtg aca gtg cag aac ccc ggc gcg	391
Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly Ala	
18 23 28 33	

gcc ctt gac ctt tgc att gca gct gta att aaa gaa tgc cat ctc gtc	439
Ala Leu Asp Leu Cys Ile Ala Ala Val Ile Lys Glu Cys His Leu Val	
34 39 44 49	

ata ctg tcg ctg aag agc caa acc tta gat gca gaa aca gat gtg tta	487
Ile Leu Ser Leu Lys Ser Gln Thr Leu Asp Ala Glu Thr Asp Val Leu	
50 55 60 65	

tgt gca gtc ctt tac agc aat cac aac aga atg ggc cgc cac aaa ccc	535
Cys Ala Val Leu Tyr Ser Asn His Asn Arg Met Gly Arg His Lys Pro	
66 71 76 81	

cat ttg gcc ctc aaa cag gtt gag caa tgt tta aag cgt ttg aaa aac		583
His Leu Ala Leu Lys Gln Val Glu Gln Cys Leu Lys Arg Leu Lys Asn		
82 87 92 97		
atg aat ttg gag ggc tca att caa gac ctg ttt gag ttg ttt tct tcc		631
Met Asn Leu Glu Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser Ser		
98 103 108 113		
aat gaa aat cag ccc tta act acc aaa gta tgt gtt gtc ccc agt cag		679
Asn Glu Asn Gln Pro Leu Thr Thr Lys Val Cys Val Val Pro Ser Gln		
114 119 124 129		
cca gtg gtg gag ttg gtg atg aag gtt ttg gga gcc tgc aag ttg		727
Pro Val Val Glu Leu Val Leu Met Lys Val Leu Gly Ala Cys Lys Leu		
130 135 140 145		
ttg ctc cgc ttg ttg gac tgc tgc tgc aaa act ttt ctt ttg act gtg		775
Leu Leu Arg Leu Leu Asp Cys Cys Lys Thr Phe Leu Leu Thr Val		
146 151 156 161		
aaa cat cta ggt ttg caa gag ttc att att tta aac ctt gtg atg gtt		823
Lys His Leu Gly Leu Gln Glu Phe Ile Ile Leu Asn Leu Val Met Val		
162 167 172 177		
ggg ctg gtg agc agg tta tgg gtt ctc tat aaa ggt gtc tta aaa agg		871
Gly Leu Val Ser Arg Leu Trp Val Leu Tyr Lys Gly Val Leu Lys Arg		
178 183 188 193		
ttg att ttg tta tat gag cct ttg ttt gga ttg ctt caa gag gtc gct		919
Leu Ile Leu Leu Tyr Glu Pro Leu Phe Gly Leu Leu Gln Glu Val Ala		
194 199 204 209		
agg att caa cca atg cct tac aaa gat ttt acc ttt cct tct gat		967
Arg Ile Gln Pro Met Pro Tyr Phe Lys Asp Phe Thr Phe Pro Ser Asp		
210 215 220 225		
atc act gaa ttt tta gga cag cca tat ttt gaa gcc ttt aag aaa aaa		1015
Ile Thr Glu Phe Leu Gly Gln Pro Tyr Phe Glu Ala Phe Lys Lys Lys		
226 231 236 241		
atg cct ata gct ttt gca gct aaa gga ata aat aaa ttg cta aat aaa		1063
Met Pro Ile Ala Phe Ala Ala Lys Gly Ile Asn Lys Leu Leu Asn Lys		
242 247 252 257		
ctg ttt tta ata aat gag cag tca cca aga gcc agt gaa gaa acc ttg		1111
Leu Phe Leu Ile Asn Glu Gln Ser Pro Arg Ala Ser Glu Glu Thr Leu		
258 263 268 273		
ctt gga att tca aaa aaa gct aaa caa atg aag atc aat gta cag aat		1159
Leu Gly Ile Ser Lys Lys Ala Lys Gln Met Lys Ile Asn Val Gln Asn		
274 279 284 289		
aat gtg gat ctt gga cag cca gta aag aat aag aga gtc ttc aaa gaa		1207
Asn Val Asp Leu Gly Gln Pro Val Lys Asn Lys Arg Val Phe Lys Glu		
290 295 300 305		
gag tca tca gaa ttt gat gtg agg gct ttc tgc aac cag ctg aaa cac		1255

Glu Ser Ser Glu Phe Asp Val Arg Ala Phe Cys Asn Gln Leu Lys His			
306	311	316	321
aaa gct act cag gag acc agt ttt gat ttt aaa tgt tct caa tcc aga			1303
Lys Ala Thr Gln Glu Thr Ser Phe Asp Phe Lys Cys Ser Gln Ser Arg			
322	327	332	337
ctt aag aca acc aag tat tct tct cag aaa gtg ata gga act cct cat			1351
Leu Lys Thr Thr Lys Tyr Ser Ser Gln Lys Val Ile Gly Thr Pro His			
338	343	348	353
gcc aaa agt ttt gtg caa aga ttc cga gag gct gag tcc ttc aca caa			1399
Ala Lys Ser Phe Val Gln Arg Phe Arg Glu Ala Glu Ser Phe Thr Gln			
354	359	364	369
ctt tct gaa gaa atc cag atg gca gtt gta tgg tgc agg agc aaa aaa			1447
Leu Ser Glu Glu Ile Gln Met Ala Val Val Trp Cys Arg Ser Lys Lys			
370	375	380	385
ctc aag gct cag gcc att ttt ctg ggt aac aaa ctt ctt aaa agc aac			1495
Leu Lys Ala Gln Ala Ile Phe Leu Gly Asn Lys Leu Leu Lys Ser Asn			
386	391	396	401
cgg ctt aaa cat ctg gaa gct caa ggt act agt ttg cca aag aaa cta			1543
Arg Leu Lys His Leu Glu Ala Gln Gly Thr Ser Leu Pro Lys Lys Leu			
402	407	412	417
gag tgc ata aaa acg tct att tgc aac cac ctt ctt cgt ggc tca ggt			1591
Glu Cys Ile Lys Thr Ser Ile Cys Asn His Leu Leu Arg Gly Ser Gly			
418	423	428	433
atc aaa act tca aag cat cat ctg aga cag aga aga tca cag aat aaa			1639
Ile Lys Thr Ser Lys His His Leu Arg Gln Arg Arg Ser Gln Asn Lys			
434	439	444	449
ttt tta cgg aga caa agg aaa cca cag aga aag ttg cag tcg act ctt			1687
Phe Leu Arg Arg Gln Arg Lys Pro Gln Arg Lys Leu Gln Ser Thr Leu			
450	455	460	465
tta agg gaa att cag cag ttc tct caa ggg act cgg aag agt gct aca			1735
Leu Arg Glu Ile Gln Gln Phe Ser Gln Gly Thr Arg Lys Ser Ala Thr			
466	471	476	481
gat acc agt gct aag tgg aga ctc tca cac tgt act gtg cat aga act			1783
Asp Thr Ser Ala Lys Trp Arg Leu Ser His Cys Thr Val His Arg Thr			
482	487	492	497
gat ctc tac cct aac agt aag cag ctc ttg aat agt gga gtt tca atg			1831
Asp Leu Tyr Pro Asn Ser Lys Gln Leu Leu Asn Ser Gly Val Ser Met			
498	503	508	513
cct gtc ata caa act aag gag aaa atg att cat gaa aat ctt aga ggc			1879
Pro Val Ile Gln Thr Lys Glu Lys Met Ile His Glu Asn Leu Arg Gly			
514	519	524	529
atc cat gaa aat gaa act gat tcg tgg acg gtg atg caa ata aat aaa			1927
Ile His Glu Asn Glu Thr Asp Ser Trp Thr Val Met Gln Ile Asn Lys			

530	535	540	545	
aac agt aca tca gga acc att aag gag aca gat gac att gat gat att				1975
Asn Ser Thr Ser Gly Thr Ile Lys Glu Thr Asp Asp Ile Asp Asp Ile				
546	551	556	561	
ttt gct tta atg gga gtt tag at gttcggtcat atgtgagact tttaagtgtat				2028
Phe Ala Leu Met Gly Val *				
562	567			
taacaaggct agttcagtgt tctaagtaga actgctaaga tctggaagta ccacctggac				2088
tcacagagga gctgcttttag tgcagcattg cacaggagtt catttcagtt cagtcatacat				2148
ttaaaagtgc attgtgtcat ttcataaca agtatttctt ttttggcttc aactacatgt				2208
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aatcgttgc aaaaaccatt gtgtcttgag gtaaatgagg agcgggggtg ggagatagca				2388
aggaaacacc tgaaaggtca atttggcttt attggctcca ttatacatag gtccgcctct				2448
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cagaaacctg catttttaac atggagccca agtgattttg atccaggtgg cccccaatc				3288
cagttatata aacactactt tagttctctc ctgtttttttttaact ggtttaattc				3348
ttaatctgta gtcagtttc atattcctga/attccaccac actggacttag tggatccgag				3408
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cttcccagtc ccacgcgtt actcgatgaa ggcagcctcc caccgggctc ctggccccgc 180

ccgagcccca ccccctgctc cttccggcc cggactgggt cccatcgccc cacctccggt 240

cgctggacgt gctctcgct agctccgcct ttcgtaagtc ccccccgcgc gc atg 295
Met 1

atg gct gcg gtg ccg ccg ggc ctg gag ccg tgg aac cgt gtg aga atc 343
Met Ala Ala Val Pro Pro Gly Leu Glu Pro Trp Asn Arg Val Arg Ile
2 7 12 17

cct aag gcg ggg aac cgc agc gca gtg aca gtg cag aac ccc ggc gcg 391
Pro Lys Ala Gly Asn Arg Ser Ala Val Thr Val Gln Asn Pro Gly Ala
18 23 28 33

gcc ttg gtt gag caa tgt tta aag cgt ttg aaa aac atg aat ttg gag 439
Ala Leu Val Glu Gln Cys Leu Lys Arg Leu Lys Asn Met Asn Leu Glu
34 39 44 49

ggc tca att caa gac ctg ttt gag ttg ttt tct tcc aat gaa aat cag 487
Gly Ser Ile Gln Asp Leu Phe Glu Leu Phe Ser Ser Asn Glu Asn Gln
50 55 60 65

ccc tta act acc aaa gta tgt gtt gtc ccc agt cag cca gtg gtg gag 535
Pro Leu Thr Thr Lys Val Cys Val Val Pro Ser Gln Pro Val Val Glu
66 71 76 81

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Leu Val Leu Met Lys Val Leu Gly Ala Cys Lys Leu Leu Leu Arg Leu
82 87 92 97

ttg gac tgc tgc aaa act ttt ctt ttg act gtg aaa cat cta ggt	631
Leu Asp Cys Cys Cys Lys Thr Phe Leu Leu Thr Val Lys His Leu Gly	
98 103 108 113	
ttg caa gag ttc att att tta aac ctt gtg atg gtt ggg ctg gtg agc	679
Leu Gln Glu Phe Ile Ile Leu Asn Leu Val Met Val Gly Leu Val Ser	
114 119 124 129	
agg tta tgg gtt ctc tat aaa ggt gtc tta aaa agg ttg att ttg tta	727
Arg Leu Trp Val Leu Tyr Lys Gly Val Leu Lys Arg Leu Ile Leu Leu	
130 135 140 145	
tat gag cct ttg ttt gga ttg ctt caa gag gtc gct agg att caa cca	775
Tyr Glu Pro Leu Phe Gly Leu Leu Gln Glu Val Ala Arg Ile Gln Pro	
146 151 156 161	
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Met Pro Tyr Phe Lys Asp Phe Thr Phe Pro Ser Asp Ile Thr Glu Phe	
162 167 172 177	
tta gga cag cca tat ttt gaa gcc ttt aag aaa aaa atg cct ata gct	871
Leu Gly Gln Pro Tyr Phe Glu Ala Phe Lys Lys Lys Met Pro Ile Ala	
178 183 188 193	
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Phe Ala Ala Lys Gly Ile Asn Lys Leu Leu Asn Lys Leu Phe Leu Ile	
194 199 204 209	
aat gag cag tca cca aga gcc agt gaa gaa acc ttg ctt gga att tca	967
Asn Glu Gln Ser Pro Arg Ala Ser Glu Glu Thr Leu Leu Gly Ile Ser	
210 215 220 225	
aaa aaa gct aaa caa atg aag atc aat gta cag aat aat gtg gat ctt	1015
Lys Lys Ala Lys Gln Met Lys Ile Asn Val Gln Asn Asn Val Asp Leu	
226 231 236 241	
gga cag cca gta aag aat aag aga gtc ttc aaa gaa gag tca tca gaa	1063
Gly Gln Pro Val Lys Asn Lys Arg Val Phe Lys Glu Glu Ser Ser Glu	
242 247 252 257	
ttt gat gtg agg gct ttc tgc aac cag ctg aaa cac aaa gct act cag	1111
Phe Asp Val Arg Ala Phe Cys Asn Gln Leu Lys His Lys Ala Thr Gln	
258 263 268 273	
gag acc agt ttt gat ttt aaa tgt tct caa tcc aga cta aag aca acc	1159
Glu Thr Ser Phe Asp Phe Lys Cys Ser Gln Ser Arg Leu Lys Thr Thr	
274 279 284 289	
aag tat tct tct cag aaa gtg ata gga act cct cat gcc aaa agt ttt	1207
Lys Tyr Ser Ser Gln Lys Val Ile Gly Thr Pro His Ala Lys Ser Phe	
290 295 300 305	
gtg caa aga ttc cga gag gct gag tcc ttc aca caa ctt tct gaa gaa	1255
Val Gln Arg Phe Arg Glu Ala Glu Ser Phe Thr Gln Leu Ser Glu Glu	
306 311 316 321	
atc cag atg gca gtt gta tgg tgc agg agc aaa aaa ctc aag gct cag	1303

Ile Gln Met Ala Val Val Trp Cys Arg Ser Lys Lys Leu Lys Ala Gln			
322	327	332	337
gcc att ttt ctg ggt aac aaa ctt ctt aaa agc aac cgg ctt aaa cat			1351
Ala Ile Phe Leu Gly Asn Lys Leu Leu Lys Ser Asn Arg Leu Lys His			
338	343	348	353
ctg gaa gct caa ggt act agt ttg cca aag aaa cta gag tgc ata aaa			1399
Leu Glu Ala Gln Gly Thr Ser Leu Pro Lys Lys Leu Glu Cys Ile Lys			
354	359	364	369
acg tct att tgc aac cac ctt ctt cgt ggc tca ggt atc aaa act tca			1447
Thr Ser Ile Cys Asn His Leu Leu Arg Gly Ser Gly Ile Lys Thr Ser			
370	375	380	385
aag cat cat ctg aga cag aga aga tca cag aat aaa ttt tta cgg aga			1495
Lys His His Leu Arg Gln Arg Arg Ser Gln Asn Lys Phe Leu Arg Arg			
386	391	396	401
caa agg aaa cca cag aga aag ttg cag tcg act ctt tta agg gaa att			1543
Gln Arg Lys Pro Gln Arg Lys Leu Gln Ser Thr Leu Leu Arg Glu Ile			
402	407	412	417
cag cag ttc tctcaa ggg act cgg aag agt gct aca gat acc agt gct			1591
Gln Gln Phe Ser Gln Gly Thr Arg Lys Ser Ala Thr Asp Thr Ser Ala			
418	423	428	433
aag tgg aga ctc tca cac tgt act gtg cat aga act gat ctc tac cct			1639
Lys Trp Arg Leu Ser His Cys Thr Val His Arg Thr Asp Leu Tyr Pro			
434	439	444	449
aac agt aag cag ctc ttg aat agt gga gtt tca atg cct gtc ata caa			1687
Asn Ser Lys Gln Leu Leu Asn Ser Gly Val Ser Met Pro Val Ile Gln			
450	455	460	465
act aag gag aaa atg att cat gaa aat ctt aga ggc atc cat gaa aat			1735
Thr Lys Glu Lys Met Ile His Glu Asn Leu Arg Gly Ile His Glu Asn			
466	471	476	481
gaa act gat tcg tgg acg gtg atg caa ata aat aaa aac agt aca tca			1783
Glu Thr Asp Ser Trp Thr Val Met Gln Ile Asn Lys Asn Ser Thr Ser			
482	487	492	497
gga acc att aag gag aca gat gac att gat gat att ttt gct tta atg			1831
Gly Thr Ile Lys Glu Thr Asp Asp Ile Asp Asp Ile Phe Ala Leu Met			
498	503	508	513
gga gtt tag atgttcg ttcatatgtg agactttaa gtgattaaca aggctagttc			1887
Gly Val *			
514			
agtgttctaa gtagaactgc taagatctgg aagtaccacc tggactcaca gaggagctgc			1947
tttagtgcag cattgcacag gagttcattt cagttcagtc tacattnaa gtgcattgt			2007
gtcatttcat caacaagtat ttcttttg gttcaacta catgtcaggt gttaatatga			2067

aaaatctgcc acagcctacc cttgagaagc agatgttaatt ccttgagtga ggcttagtaag	2127
tctctgaaaa actgaataat tttatgactt actaggcaat ttaataatcg tttgcaaaaa	2187
ccattgtgtc ttgaggtaaa tgaggagcgg ggggtggaga tagcaaggaa acacctgaaa	2247
ggtcaatttg gtcttattgg ctccattata cataggtccg cctctgaata ctaaagtttgc	2307
tagctcctga catttatgtt ttcttgtta tatgttgaa ttgatcaaca aggtttgcca	2367
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tcatattaaa gtgagtttgg agttctccaa aacgtttaa ttttattttat ttgggttacca	2487
gtgattgatt ccaaataaac ctttttacaa aaaggcaata aggtggtttta tggttacata	2547
tgaaatataa taggataaca ggttagatgag aaagtaaaat gaaaaaatga ggtaggaga	2607
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tgatagggga tggctcggt actgttgctc tgaggggagt acatcttgag tattttcaaa	2727
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tttcccttcc attcttatt tggcttggc cttccctgt ctgccttctc cattttctca	2967
gttatctcta ccagtggttc tcaaacttta gacttttga gaatcacctg gtgggttgct	3027
aaaagatgca gattagccct ttcccagaga ctgataaaaca ggggcccagaa acctgcattt	3087
ttaacatgga gcccagtga ttttgcatttca ggtggccccc aaatccagtt atataaacac	3147
tacttttagct tctctccttgc agccttaagt aaactggttt aattcttaat ctgttagtcag	3207
ttttcatatt cctgaattcc accacactgg actagtggat ccgagctcgg taccacgttt	3267
aagtttaaac gctagccagc ttgggtctcg caacccaaaan nnggggnttc aa	3319

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60

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cggttgcgg ccggcagttt ccgtgggtct gtgaagaggt cggcggcccc tgccggcgcc	180
agtcagctt aagaaaaagt agagatcact tctgactgta ctgaacagca aaaattaagt	240
gacttgcgc cctgcacatc atg gca ctg cca ttc cgt aag gac tta gaa Met Ala Leu Pro Phe Arg Lys Asp Leu Glu	290
1 5	
aag tac aaa gac ctt gat gaa gat gag ctc ctt ggg aat ctg tca gaa Lys Tyr Lys Asp Leu Asp Glu Leu Leu Gly Asn Leu Ser Glu	338
11 16 21 26	
aca gaa ctg aaa caa ctg gaa act gtt ttg gat gat ctt gac ccc gag Thr Glu Leu Lys Gln Leu Glu Thr Val Leu Asp Asp Leu Asp Pro Glu	386
27 32 37 42	
aat gcc ctt ctg cct gca ggg ttc cgg cag aag aac cag aca tca aag Asn Ala Leu Leu Pro Ala Gly Phe Arg Gln Lys Asn Gln Thr Ser Lys	434
43 48 53 58	
tcc acc aca ggg cca ttt gat aga gag cat ctc ctt tca tat ctg gag Ser Thr Thr Gly Pro Phe Asp Arg Glu His Leu Leu Ser Tyr Leu Glu	482
59 64 69 74	
aaa gaa gca ttg gag cat aaa gac agg gaa gac tat gtg ccc tac act Lys Glu Ala Leu Glu His Lys Asp Arg Glu Asp Tyr Val Pro Tyr Thr	530
75 80 85 90	
gga gaa aaa aaa ggg aaa ata ttt atc ccc aaa cag aaa cct gta cag Gly Glu Lys Lys Gly Lys Ile Phe Ile Pro Lys Gln Lys Pro Val Gln	578
91 96 101 106	
act ttt aca gaa gaa aaa gtg tct ctt gat cca gaa tta gaa gaa gct Thr Phe Thr Glu Glu Lys Val Ser Leu Asp Pro Glu Leu Glu Glu Ala	626
107 112 117 122	
ttg aca agt gct tct gat aca gaa ttg tgt gac ctc gca gca att ctt Leu Thr Ser Ala Ser Asp Thr Glu Leu Cys Asp Leu Ala Ala Ile Leu	674
123 128 133 138	
ggg atg cac aat ttg ata acg aat aca aag ttc tgt aat ata atg gga Gly Met His Asn Leu Ile Thr Asn Thr Lys Phe Cys Asn Ile Met Gly	722
139 144 149 154	
agt agt aat ggt gtt gac caa gaa cat ttt tca aat gtg gtc aaa ggt Ser Ser Asn Gly Val Asp Gln Glu His Phe Ser Asn Val Val Lys Gly	770
155 160 165 170	
gaa aag att ctt ccg gta ttt gat gag cca cca aat cca acc aat gta Glu Lys Ile Leu Pro Val Phe Asp Glu Pro Pro Asn Pro Thr Asn Val	818
171 176 181 186	
gaa gag agt ttg aag aga act aaa gaa aac gat gct cat ctt gtt gaa Glu Glu Ser Leu Lys Arg Thr Lys Glu Asn Asp Ala His Leu Val Glu	866
187 192 197 202	

gtt aat ttg aat aat ata aag aat atc cca att cca acc cta aaa gat Val Asn Leu Asn Asn Ile Lys Asn Ile Pro Ile Pro Thr Leu Lys Asp 203 208 213 218	914
ttt gca aag gct ttg gaa acc aac aca cat gtg aaa tgt ttc agt ctt Phe Ala Lys Ala Leu Glu Thr Asn Thr His Val Lys Cys Phe Ser Leu 219 224 229 234	962
gca gcc acc cgg agc aat gac cct gtt gct act gct ttt gca gaa atg Ala Ala Thr Arg Ser Asn Asp Pro Val Ala Thr Ala Phe Ala Glu Met 235 240 245 250	1010
ctg aaa gtg aac aaa act ttg aag agc tta aat gtg gag tcc aac ttt Leu Lys Val Asn Lys Thr Leu Lys Ser Leu Asn Val Glu Ser Asn Phe 251 256 261 266	1058
atc acg gga gtt ggg att ctg gca ctg att gat gcg tta aga gat aat Ile Thr Gly Val Gly Ile Leu Ala Leu Ile Asp Ala Leu Arg Asp Asn 267 272 277 282	1106
gaa acc ctg gca gag ctc aag att gac aat cag agg cag cag ttg ggg Glu Thr Leu Ala Glu Leu Lys Ile Asp Asn Gln Arg Gln Gln Leu Gly 283 288 293 298	1154
aca gct gta gaa ttg gaa atg gcc aag atg ctt gag gaa aat aca aat Thr Ala Val Glu Leu Glu Met Ala Lys Met Leu Glu Glu Asn Thr Asn 299 304 309 314	1202
atc ctt aaa ttt gga tat cag ttt aca cag cag gga cca cga acc aga Ile Leu Lys Phe Gly Tyr Gln Phe Thr Gln Gln Gly Pro Arg Thr Arg 315 320 325 330	1250
gca gct aat gct ata aca aaa aac aat gac tta gtg cgt aag aga cga Ala Ala Asn Ala Ile Thr Lys Asn Asn Asp Leu Val Arg Lys Arg Arg 331 336 341 346	1298
gtt gaa gga gat cac cag taa gt ctgcaaaggt gtaatcttg gaagacttca Val Glu Gly Asp His Gln *347 352	1351
gaagatcacc aagggtcat gttggtgaca tcatgtaaaa tttcctggg tagaaggaa aagactggaa aaattttttt agtgacatgc atttttttt tagttgttat caaattgtaa aatcagtaat gtgatattt atattctgaa acattctac tttctgctaa aatcaatttt aatttagtt aattgaatga tttatgatga atcttggca aaaaaataca actgtaaaaaa atttcacagg tcattgtgt agaataattt gaacattgtg aggaccaatc tttttaaat caaaaggat gttgctggta tcagaattgt tattgctca ttttagacata aaacacttaa gtgtttcct tcactccgtg acctggagag tttccattt tttgcaagtt tagtaactgcc caaatttact cattctacag tgtaactgca ctttgaacgt attgaccat gtcacccaaag	1411 1471 1531 1591 1651 1711 1771 1831

agaagcaaac atatggatgc actagagaca actcggttg ctgctctcg ttaaggcgt	1891
tgagttcttg gggctaaatc atctgtaaaa ttatcctctc catcagctct cactgatcat	1951
taatgtttct ggatatttct taccctaaga tttgcttacc aacaaatcaa agaaacgctt	2011
cactaattat tttaaatttg agaaaatagt attcagaggc aaagattttt atattctttt	2071
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gttggccgct gctgctagca cgttgaaccc cagggtcggg accg atg tcg gct tgg 116
Met Ser Ala Trp

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gct gct gcc agc cta agc agg gcc gct gcc gaa tgc ttg ctg gca cga      164
Ala Ala Ala Ser Leu Ser Arg Ala Ala Ala Glu Cys Leu Leu Ala Arg
      5           10           15           20

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ggc ccc ggg gtc agg gcg gct cct ccg cgc gac ccc cgg ccc tcc cac 212
Gly Pro Gly Val Arg Ala Ala Pro Pro Arg Asp Pro Arg Pro Ser His
 21           .       26           .       31           .       36

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ccc gag ccc cgg ggc tgc ggt gcc gct ccg ggc agg acg ctg cac ttt 260
 Pro Glu Pro Arg Gly Cys Gly Ala Ala Pro Gly Arg Thr Leu His Phe
 37 42 47 52

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acc gcg gct gtc ccc gcc ggg cac aac aag tgg tcc aaa gtc agg cac 308
Thr Ala Ala Val Pro Ala Gly His Asn Lys Trp Ser Lys Val Arg His
53           58           63           68

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atc aag ggt ccg aag gac gtc gaa agg agt cgc atc ttc tcc aaa ctc 356
 Ile Lys Gly Pro Lys Asp Val Glu Arg Ser Arg Ile Phe Ser Lys Leu
 69 74 79 84

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tgt ttg aac atc cgc ctg gca gtg aaa gaa gga ggc ccc aac cct gag 404
Cys Leu Asn Ile Arg Leu Ala Val Lys Glu Gly Gly Pro Asn Pro Glu
 85           90           95           100
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cac aac agc aac ctg gcc aat atc tta gag gtg tgt cgc agc aaa cat 452
 His Asn Ser Asn Léu Ala Asn Ile Leu Glu Val Cys Arg Ser Lys His
 101 106 111 116

atg ccc aag tca acg att gag aca gca ctg aaa atg gag aaa tcc aag Met Pro Lys Ser Thr Ile Glu Thr Ala Leu Lys Met Glu Lys Ser Lys 117 122 127 132	500
gac act tat ttg ctg tat gag ggt cga ggc cct ggt ggc tct tct ctg Asp Thr Tyr Leu Leu Tyr Glu Gly Arg Gly Pro Gly Gly Ser Ser Leu 133 138 143 148	548
ctc atc gag gca tta tct aac agt agc cac aag tgc caa gca gac att Leu Ile Glu Ala Leu Ser Asn Ser Ser His Lys Cys Gln Ala Asp Ile 149 154 159 164	596
aga cat atc ctg aat aag aat gga gga gtg atg gct gta gga gct cgt Arg His Ile Leu Asn Lys Asn Gly Gly Val Met Ala Val Gly Ala Arg 165 170 175 180	644
cac tct ttt gac aaa aag ggg gtg att gtg gtt gaa gtg gag gac aga His Ser Phe Asp Lys Lys Gly Val Ile Val Val Glu Val Glu Asp Arg 181 186 191 196	692
gag aag aag gct gtg aac cta gag cgt gcc ctg gag atg gca atc gaa Glu Lys Lys Ala Val Asn Leu Glu Arg Ala Leu Glu Met Ala Ile Glu 197 202 207 212	740
gca gga gct gag gat gtc aag gaa act gaa gat gaa gaa agg aac Ala Gly Ala Glu Asp Val Lys Glu Thr Glu Asp Glu Glu Arg Asn 213 218 223 228	788
gtt ttt aaa ttt att tgt gat gcc tct tca ctg cac caa gtg agg aag Val Phe Lys Phe Ile Cys Asp Ala Ser Ser Leu His Gln Val Arg Lys 229 234 239 244	836
aag ctg gac tcc ctg ggc ctg tgt tct gtg tcc tgt gca cta gag ttc Lys Leu Asp Ser Leu Gly Leu Cys Ser Val Ser Cys Ala Leu Glu Phe 245 250 255 260	884
atc ccc aac tca aag gtg cag ctg gct gag ccc gac ctg gaa cag gcc Ile Pro Asn Ser Lys Val Gln Leu Ala Glu Pro Asp Leu Glu Gln Ala 261 266 271 276	932
gca cat ctc att cag gct ctc agc aac cac gag gat gtg att cac gtc Ala His Leu Ile Gln Ala Leu Ser Asn His Glu Asp Val Ile His Val 277 282 287 292	980
tat gat aac att gaa taa ccaggc tacatgtgcc cccgggttcc ttccctagaaa Tyr Asp Asn Ile Glu *293 298	1034
tgtggcagcc cattccagca cacaggcttc tgcagcaatc tctgagggtta aagccgggtgg gaggctcagc aggccaggag gccccaggac aggacttgcg accttgaagc caaaggaatc tcacttgtgg ggcctccttg tcagctctgc tgctgtctca gagccatctg gatgagtgtc ccgacaccct ctcggatgca gggcaggacc acccagctgg tcagactctg atgttgggt gctggcctct gtggggattt taagtgcctt gaggcgctct gtactagaaa ctgcctttaa	1094 1154 1214 1274 1334

taataacgggt gattattgggt tgctgcaaaa aaaaaaaaa

1372

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<400> 579

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gccgactgtg tggcagctga ggaagagttt tgcacgtgga tcgcccgttcg ggtggggcgag 120

atg gag aca gcc ccc aag ccg ggc aag gat gtc ccg ccc aag aaa gac 168
Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp
1 5 10 15

aaa ctt cag acc aag aga aag aaa ccg ccg cga tac tgg gag gaa gag 216
Lys Leu Gln Thr Lys Arg Lys Pro Arg Arg Tyr Trp Glu Glu Glu
17 22 27 32

acc gtt ccg acc aca gcc gga gcc tct cca ggg cct cct cgt aac aag 264
Thr Val Pro Thr Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys
33 38 43 48

aag aat ccg gag ctc cgt cct cag aga cca aaa aat gct tac atc tta 312
Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu
49 54 59 64

aag aag tct ccg atc tct aag aag cct cag gtc ccg aag aaa ccc cga 360
Lys Lys Ser Arg Ile Ser Lys Pro Gln Val Pro Lys Lys Pro Arg
65 70 75 80

gaa tgg aag aac ccg gag tcc cag ccg ggc ttg tcc ggg gcc caa gat 408
Glu Trp Lys Asn Pro Glu Ser Gln Arg Gly Leu Ser Gly Ala Gln Asp
81 86 91 96

cca ttc cca ggc ccc gcc ccc gtc cct gtg gaa gtg gtc cag aag ttc 456
Pro Phe Pro Gly Pro Ala Pro Val Pro Val Glu Val Val Gln Lys Phe
97 102 107 112

tgt cgc att gac aaa tcc cga aag cta cca cat tct aaa gcc aaa act 504
Cys Arg Ile Asp Lys Ser Arg Lys Leu Pro His Ser Lys Ala Lys Thr
113 118 123 128

cga agc cga ctt gag gtg gct gaa gct gag gaa gag gaa aca agt atc		552	
Arg Ser Arg Leu Glu Val Ala Glu Ala Glu Glu Glu Thr Ser Ile			
129	134	139	144
aaa gct gct cgt tct gag ctg ctg ctt gct gaa gaa cct ggg ttt ctg		600	
Lys Ala Ala Arg Ser Glu Leu Leu Ala Glu Glu Pro Gly Phe Leu			
145	150	155	160
gaa ggg gag gat ggg gaa gac aca gca aag ata tgc cag gct gac att		648	
Glu Gly Glu Asp Gly Glu Asp Thr Ala Lys Ile Cys Gln Ala Asp Ile			
161	166	171	176
gtg gag gct gtg gac att gca agt gca gcc aag cac ttt gac ttg aat		696	
Val Glu Ala Val Asp Ile Ala Ser Ala Ala Lys His Phe Asp Leu Asn			
177	182	187	192
ctg cgg cag ttt gga ccc tac aga cta aac tac tct cga act gga aga		744	
Leu Arg Gln Phe Gly Pro Tyr Arg Leu Asn Tyr Ser Arg Thr Gly Arg			
193	198	203	208
cac ctg gct ttt gga ggg cgc cga ggt cat gtg gct gcc ctt gat tgg		792	
His Leu Ala Phe Gly Arg Arg Gly His Val Ala Ala Leu Asp Trp			
209	214	219	224
gta aca aag aag ctt atg tgc gag atc aac gtc atg gag gcg gtg cgg		840	
Val Thr Lys Lys Leu Met Cys Glu Ile Asn Val Met Glu Ala Val Arg			
225	230	235	240
gac atc cgg ttt ctc cat tct gag gca ctg ctt gct gtt gct cag aac		888	
Asp Ile Arg Phe Leu His Ser Glu Ala Leu Leu Ala Val Ala Gln Asn			
241	246	251	256
cgc tgg ctc cac atc tat gac aat cag ggc att gag ctc cac tgt atc		936	
Arg Trp Leu His Ile Tyr Asp Asn Gln Gly Ile Glu Leu His Cys Ile			
257	262	267	272
cgc cgc tgt gac cga gta aca cgg ctt gag ttc ctg ccc ttc cac ttc		984	
Arg Arg Cys Asp Arg Val Thr Arg Leu Glu Phe Leu Pro Phe His Phe			
273	278	283	288
ctc ctg gct aca gct tca gaa aca ggg ttt cta acc tac ctg gat gtg		1032	
Leu Leu Ala Thr Ala Ser Glu Thr Gly Phe Leu Thr Tyr Leu Asp Val			
289	294	299	304
tca gtg ggg aag att gtg gca gct ctg aat gct cga gct ggg cgg ctc		1080	
Ser Val Gly Lys Ile Val Ala Ala Leu Asn Ala Arg Ala Gly Arg Leu			
305	310	315	320
gat gtt atg agt cag aac cct tac aat gcc gtc atc cat ctc gga cac		1128	
Asp Val Met Ser Gln Asn Pro Tyr Asn Ala Val Ile His Leu Gly His			
321	326	331	336
agc aat ggt act gtg tct tta tgg agt cca gct atg aag gag cca ctg		1176	
Ser Asn Gly Thr Val Ser Leu Trp Ser Pro Ala Met Lys Glu Pro Leu			
337	342	347	352
gca aag att ctc tgt cat cgt ggt ggg gtc cgg gct gtg gca gta gat		1224	

Ala Lys Ile Leu Cys His Arg Gly Gly Val Arg Ala Val Ala Val Asp			
353	358	363	368
tct aca ggc acg tac atg gcc acc tct ggc cta gac cac cag ctg aag			1272
Ser Thr Gly Thr Tyr Met Ala Thr Ser Gly Leu Asp His Gln Leu Lys			
369	374	379	384
atc ttt gac ttg cga ggg acg tac cag cct ctg agc act cgg acc ctg			1320
Ile Phe Asp Leu Arg Gly Thr Tyr Gln Pro Leu Ser Thr Arg Thr Leu			
385	390	395	400
ccc cat gga gca ggg cac ctg gcc ttc tcc cag agg gga ctg ctg gtg			1368
Pro His Gly Ala Gly His Leu Ala Phe Ser Gln Arg Gly Leu Leu Val			
401	406	411	416
gcg gga atg ggt gac gtt gtc aac atc tgg gca ggg cag ggc aag gcc			1416
Ala Gly Met Gly Asp Val Val Asn Ile Trp Ala Gly Gln Gly Lys Ala			
417	422	427	432
agc cca ccc tcc ctt gaa cag ccc tac ctc acc cac cgg ctc tca ggc			1464
Ser Pro Pro Ser Leu Glu Gln Pro Tyr Leu Thr His Arg Leu Ser Gly			
433	438	443	448
cct gtg cat ggc ctt cag ttc tgc ccc ttt gaa gat gtg ctg ggg gtg			1512
Pro Val His Gly Leu Gln Phe Cys Pro Phe Glu Asp Val Leu Gly Val			
449	454	459	464
ggg cac act ggg ggc atc acc agc atg ctg gtc cct ggg gcc ggt gag			1560
Gly His Thr Gly Ile Thr Ser Met Leu Val Pro Gly Ala Gly Glu			
465	470	475	480
ccc aac ttc gat ggc ctg gag agt aat cca tac aga agc cgg aag cag			1608
Pro Asn Phe Asp Gly Leu Glu Ser Asn Pro Tyr Arg Ser Arg Lys Gln			
481	486	491	496
cgc cag gag tgg gag gtg aag gcc ctg cta gag aag gta cct gca gag			1656
Arg Gln Glu Trp Glu Val Lys Ala Leu Leu Glu Lys Val Pro Ala Glu			
497	502	507	512
ctt att tgt ctg gac cca cga gcc ctg gcc gag gtg gat gtc atc tcc			1704
Leu Ile Cys Leu Asp Pro Arg Ala Leu Ala Glu Val Asp Val Ile Ser			
513	518	523	528
ctg gag cag gga aag aag gag cag ata gag agg ctg ggc tat gac ccg			1752
Leu Glu Gln Gly Lys Lys Glu Gln Ile Glu Arg Leu Gly Tyr Asp Pro			
529	534	539	544
cag gct aag gct ccc ttc cag cca aag cca aag cag aag ggc cgc agc			1800
Gln Ala Lys Ala Pro Phe Gln Pro Lys Pro Lys Gln Lys Gly Arg Ser			
545	550	555	560
tcc acg gca agc ctg gtg aag agg aag agg aag gtc atg gat gag gaa			1848
Ser Thr Ala Ser Leu Val Lys Arg Lys Arg Lys Val Met Asp Glu Glu			
561	566	571	576
cac agg gac aag gtc cgg cag agc ctt cag cag cag cat cat aag gag			1896
His Arg Asp Lys Val Arg Gln Ser Leu Gln Gln His His Lys Glu			

577	582	587	592	
gct aag gcc aag ccc acg ggg gcc cgg cca tct gcc ctg gac aga ttt				1944
Ala Lys Ala Lys Pro Thr Gly Ala Arg Pro Ser Ala Leu Asp Arg Phe				
593	598	603	608	
gtg cgc tga gccagac tccagggttg cctggaaaca gtctctcccc aagatcacct				2000
Val Arg *				
609				
gtaggaaat gagtgttccc tggaacaagg aggtggggc agtgtggccc cttccccaac				2060
tgggggtgga cagctgtctc ctgggtggg ttggtattaa agagggaaagc gatTTTTGG				2120
aaaaaaaaaaa aaaaggggggg gccgtttaa aggttccttg ggggggccc agtttacccg				2180
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atg gag aca gcc ccc aag ccg ggc aag gat gtc ccg ccc aag aaa gac		168		
Met Glu Thr Ala Pro Lys Pro Gly Lys Asp Val Pro Pro Lys Lys Asp				
1	5	10	15	
aaa ctt cag acc aag aga aag aaa ccg ccg cga tac tgg gag gaa gag		216		
Lys Leu Gln Thr Lys Arg Lys Pro Arg Arg Tyr Trp Glu Glu Glu				
17	22	27	32	
acc gtt ccg acc aca gcc gga gcc tct cca ggg cct cct cgt aac aag		264		
Thr Val Pro Thr Ala Gly Ala Ser Pro Gly Pro Pro Arg Asn Lys				
33	38	43	48	
aag aat ccg gag ctc cgt cct cag aga cca aaa aat gct tac atc tta		312		
Lys Asn Arg Glu Leu Arg Pro Gln Arg Pro Lys Asn Ala Tyr Ile Leu				
49	54	59	64	
aag aag tct ccg atc tct aag aag cct cag gtc ccg aag aaa ccc cga		360		

Lys Lys Ser Arg Ile Ser Lys Lys Pro Gln Val Pro Lys Lys Pro Arg
 65 70 75 80
 gaa tgg aag aac ccg gag tcc cag cgc ggc ttg tcc ggg gcc caa gat 408
 Glu Trp Lys Asn Pro Glu Ser Gln Arg Gly Leu Ser Gly Ala Gln Asp
 81 86 91 96
 cca ttc cca ggc ccc gcc ccc gtc cct gtg gaa gtg gtc cag aag ttc 456
 Pro Phe Pro Gly Pro Ala Pro Val Pro Val Glu Val Val Gln Lys Phe
 97 102 107 112
 tgt cgc att gac aaa tcc cga aag cta cca cat tct aaa gcc aaa act 504
 Cys Arg Ile Asp Lys Ser Arg Lys Leu Pro His Ser Lys Ala Lys Thr
 113 118 123 128
 cga agc cga ctt gag gtg gct gaa gct gag gaa gag gaa aca agt atc 552
 Arg Ser Arg Leu Glu Val Ala Glu Ala Glu Glu Glu Thr Ser Ile
 129 134 139 144
 aaa gct gct cgt tct gag ctg ctg ctt gct gaa gaa cct ggg ttt ctg 600
 Lys Ala Ala Arg Ser Glu Leu Leu Leu Ala Glu Glu Pro Gly Phe Leu
 145 150 155 160
 gaa ggg gag gat ggg gaa gac aca gca aag ata tgc cag gct gac att 648
 Glu Gly Glu Asp Gly Glu Asp Thr Ala Lys Ile Cys Gln Ala Asp Ile
 161 166 171 176
 gtg gag gct gtg gac att gca agt gca gcc aag cac ttt gac ttg aat 696
 Val Glu Ala Val Asp Ile Ala Ser Ala Ala Lys His Phe Asp Leu Asn
 177 182 187 192
 ctg cgg cag ttt gga ccc tac aga cta aac tac tct cga act gga aga 744
 Leu Arg Gln Phe Gly Pro Tyr Arg Leu Asn Tyr Ser Arg Thr Gly Arg
 193 198 203 208
 cac ctg gct ttt gga ggg cgc cga ggt cat gtg gct gcc ctt gat tgg 792
 His Leu Ala Phe Gly Gly Arg Arg Gly His Val Ala Ala Leu Asp Trp
 209 214 219 224
 gta aca aag aag ctt atg tgc gag atc aac gtc atg gag gcg gtg cgg 840
 Val Thr Lys Lys Leu Met Cys Glu Ile Asn Val Met Glu Ala Val Arg
 225 230 235 240
 gac atc cgg ttt ctc cat tct gag gca ctg ctt gct gtt gct cag aac 888
 Asp Ile Arg Phe Leu His Ser Glu Ala Leu Leu Ala Val Ala Gln Asn
 241 246 251 256
 cgc tgg ctc cac atc tat gac aat cag ggc att gag ctc cac tgt atc 936
 Arg Trp Leu His Ile Tyr Asp Asn Gln Gly Ile Glu Leu His Cys Ile
 257 262 267 272
 cgc cgc tgt gac cga gta aca cgg ctt gag ttc ctg ccc ttc cac ttc 984
 Arg Arg Cys Asp Arg Val Thr Arg Leu Glu Phe Leu Pro Phe His Phe
 273 278 283 288
 ctc ctg gct aca gct tca gaa aca ggg ttt cta acc tac ctg gat gtg 1032
 Leu Leu Ala Thr Ala Ser Glu Thr Gly Phe Leu Thr Tyr Leu Asp Val

289	294	299	304														
tca	gtg	ggg	aag	att	gtg	gca	gct	ctg	aat	gct	cga	gct	ggg	cgg	ctc		1080
Ser	Val	Gly	Lys	Ile	Val	Ala	Ala	Leu	Asn	Ala	Arg	Ala	Gly	Arg	Leu		
305					310					315						320	
gat	gtt	atg	agt	cag	aac	cct	tac	aat	gcc	gtc	atc	cat	ctc	gga	cac		1128
Asp	Val	Met	Ser	Gln	Asn	Pro	Tyr	Asn	Ala	Val	Ile	His	Leu	Gly	His		
321					326					331						336	
agc	aat	ggt	act	gtg	tct	tta	tgg	agt	cca	gct	atg	aag	gag	cca	ctg		1176
Ser	Asn	Gly	Thr	Val	Ser	Leu	Trp	Ser	Pro	Ala	Met	Lys	Glu	Pro	Leu		
337					342					347						352	
gca	aag	att	ctc	tgt	cat	cgt	ggg	gtc	cgg	gct	gtg	gca	gta	gat			1224
Ala	Lys	Ile	Leu	Cys	His	Arg	Gly	Gly	Val	Arg	Ala	Val	Ala	Val	Asp		
353					358					363						368	
tct	aca	ggc	acg	tac	atg	gcc	acc	tct	ggc	cta	gac	cac	cag	ctg	aag		1272
Ser	Thr	Gly	Thr	Tyr	Met	Ala	Thr	Ser	Gly	Leu	Asp	His	Gln	Leu	Lys		
369					374					379						384	
atc	ttt	gac	ttg	cga	ggg	acg	tac	cag	cct	ctg	agc	act	cgg	acc	ctg		1320
Ile	Phe	Asp	Leu	Arg	Gly	Thr	Tyr	Gln	Pro	Leu	Ser	Thr	Arg	Thr	Leu		
385					390					395						400	
ccc	cat	gga	gca	ggg	cac	ctg	gcc	ttc	tcc	cag	agg	gga	ctg	ctg	gtg		1368
Pro	His	Gly	Ala	Gly	His	Leu	Ala	Phe	Ser	Gln	Arg	Gly	Leu	Leu	Val		
401					406					411						416	
gcg	gga	atg	ggt	gac	gtt	gtc	aac	atc	tgg	gca	ggg	cag	ggc	aag	gcc		1416
Ala	Gly	Met	Gly	Asp	Val	Val	Asn	Ile	Trp	Ala	Gly	Gln	Gly	Lys	Ala		
417					422					427						432	
agc	cca	ccc	tcc	ctt	gaa	cag	ccc	tac	ctc	acc	cac	cgg	ctc	tca	ggc		1464
Ser	Pro	Pro	Ser	Leu	Glu	Gln	Pro	Tyr	Leu	Thr	His	Arg	Leu	Ser	Gly		
433					438					443						448	
cct	gtg	cat	ggc	ctt	cag	ttc	tgc	ccc	ttt	gaa	gat	gtg	ctg	ggg	gtg		1512
Pro	Val	His	Gly	Leu	Gln	Phe	Cys	Pro	Phe	Glu	Asp	Val	Leu	Gly	Val		
449					454					459						464	
ggg	cac	act	ggg	ggc	atc	acc	agc	atg	ctg	gtc	cct	ggg	gcc	ggt	gag		1560
Gly	His	Thr	Gly	Gly	Ile	Thr	Ser	Met	Leu	Val	Pro	Gly	Ala	Gly	Glu		
465					470					475						480	
ccc	aac	ttc	gat	ggc	ctg	gag	agt	aat	cca	tac	aga	agc	cgg	aag	cag		1608
Pro	Asn	Phe	Asp	Gly	Leu	Glu	Ser	Asn	Pro	Tyr	Arg	Ser	Arg	Lys	Gln		
481					486					491						496	
cgc	cag	gag	tgg	gag	gtg	aag	gcc	ctg	cta	gag	aag	gta	cct	gca	gag		1656
Arg	Gln	Glu	Trp	Glu	Val	Lys	Ala	Leu	Leu	Glu	Lys	Val	Pro	Ala	Glu		
497					502					507						512	
ctt	att	tgt	ctg	gac	cca	cga	gcc	ctg	gcc	gag	gtg	gat	gtc	atc	tcc		1704
Leu	Ile	Cys	Leu	Asp	Pro	Arg	Ala	Leu	Ala	Glu	Val	Asp	Val	Ile	Ser		
513					518					523						528	

ctg gag cag gga aag aag gag cag agc ctt cag cag cag cat cat aag Leu Glu Gln Gly Lys Lys Glu Gln Ser Leu Gln Gln His His Lys 529 534 539 544	1752
gag gcg aag gcc aag ccc acg ggg gcc cg ^g cca tct gcc ctg gac aga Glu Ala Lys Ala Lys Pro Thr Gly Ala Arg Pro Ser Ala Leu Asp Arg 545 550 555 560	1800
ttt gtg cgc tga gcc agactccagg gttgcctggg aacagtctct ccccaagatc Phe Val Arg * 561	1855
acctgttaggg aaatgagtgt tccctggaac aaggaggtgg gggcagtgtg gccccttccc	1915
caactggggg tggacagctg tctcctgggg tgggttggta ttaaagagga aagcgatttt	1975
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cccgccatg caacgtaata gttcttccc tatagggagc cgaattat	2083

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 <212> DNA
 <213> Homo sapiens

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ctctctttt tcctccctcg ctgcgtgc ^g ggc ^t atgtc ^t t gatctggcgg c ^t cgctcctac	180
caccctggc agccgagcag agtggtcccc agcgggtctc cttccctg ^c cc tccctgactt	240
tgcaacaccg cg ^t tccggga ggaccggc ^t t cggcgaggga ggaggcgggg gagctgc ^g aa	300
cacccagacc caaaccctga catgctctgg ggcggagagg aggaagccag gagctgagcg	360
cgccgcgggg gctgcttcgc cttccggctc cgaggcggcgg gctccggcgg ccctgccttg	420
cgcctggca gcagc ^t tcgc tgg ^t cttggg ggcggccccc gcttcccgc ^c cc ggggggtcc	480
gcggccggca ggacc atg ctg ctg aaa gag tac cgg atc tgc atg ccg ctc Met Leu Leu Lys Glu Tyr Arg Ile Cys Met Pro Leu 1 5 10	531
acc gta gac gag tac aaa att gga cag ctg tac atg atc agc aaa cac Thr Val Asp Glu Tyr Lys Ile Gly Gln Leu Tyr Met Ile Ser Lys His 13 18 23 28	579

agc cat gaa cag agt gac cg ^g gga gaa ggg gtg gag gtc gtc cag aat Ser His Glu Gln Ser Asp Arg Gly Glu Gly Val Glu Val Val Gln Asn 29 34 39 44	627
gag ccc ttt gag gac cct cac cat ggc aat ggg cag ttc acc gag aag Glu Pro Phe Glu Asp Pro His His Gly Asn Gly Gln Phe Thr Glu Lys 45 50 55 60	675
cgg gtg tat ctc aac agc aaa ctg cct agt tgg gct aga gct gtt gtc Arg Val Tyr Leu Asn Ser Lys Leu Pro Ser Trp Ala Arg Ala Val Val 61 66 71 76	723
ccc aaa ata ttt tat gtg aca gag aag gct tgg aac tat tat ccc tac Pro Lys Ile Phe Tyr Val Thr Glu Lys Ala Trp Asn Tyr Tyr Pro Tyr 77 82 87 92	771
aca att aca gaa tac aca tgt tcc ttt ctg ccg aaa ttc tcc att cat Thr Ile Thr Glu Tyr Thr Cys Ser Phe Leu Pro Lys Phe Ser Ile His 93 98 103 108	819
ata gaa acc aag tat gag gac aac aaa gga agc aat gac acc att ttc Ile Glu Thr Lys Tyr Glu Asp Asn Lys Gly Ser Asn Asp Thr Ile Phe 109 114 119 124	867
gac aat gaa gcc aaa gac gtg gag aga gaa gtt tgc ttt att gat att Asp Asn Glu Ala Lys Asp Val Glu Arg Glu Val Cys Phe Ile Asp Ile 125 130 135 140	915
gcc tgc gat gaa att cca gag cgc tac tac aaa gaa tct gag gat cct Ala Cys Asp Glu Ile Pro Glu Arg Tyr Tyr Lys Glu Ser Glu Asp Pro 141 146 151 156	963
aag cac ttc aag tca gag aag aca gga cgg gga cag ttg agg gaa ggc Lys His Phe Lys Ser Glu Lys Thr Gly Arg Gly Gln Leu Arg Glu Gly 157 162 167 172	1011
tgg aga gat agt cat cag cct atc atg tgc tcc tac aag ctg gtg act Trp Arg Asp Ser His Gln Pro Ile Met Cys Ser Tyr Lys Leu Val Thr 173 178 183 188	1059
gtg aag ttt gag gtc tgg ggg ctt cag acc aga gtg gaa caa ttt gta Val Lys Phe Glu Val Trp Gly Leu Gln Thr Arg Val Glu Gln Phe Val 189 194 199 204	1107
cac aag gtg gtc cga gac att ctg ctg att gga cat aga cag gct ttt His Lys Val Val Arg Asp Ile Leu Leu Ile Gly His Arg Gln Ala Phe 205 210 215 220	1155
gca tgg gtt gat gag tgg tat gat atg aca atg gat gat gtt cgg gaa Ala Trp Val Asp Glu Trp Tyr Asp Met Thr Met Asp Asp Val Arg Glu 221 226 231 236	1203
tac gag aaa aac atg cat gaa caa acc aac ata aaa gtt tgc aat cag Tyr Glu Lys Asn Met His Glu Gln Thr Asn Ile Lys Val Cys Asn Gln 237 242 247 252	1251

cat tcc tcc cct gtg gat gac ata gag agt cat gcc caa aca agt aca	1299
His Ser Ser Pro Val Asp Asp Ile Glu Ser His Ala Gln Thr Ser Thr	
253 258 263 268	
tga caat ggatgaagtc cgagaatttg aacgagccac tcaggaagcc accaacaaga	1356
*	
269	
aaatcgccat tttcccacct gcaatttcta tctccagcat cccccctgctg ccttcttccg	1416
tccgcagtgc gccttctagt gctccatcca cccctctctc cacagacgca cccgaatttc	1476
tgtccgttcc caaagatcgg ccccgaaaaa agtctgcccc agaaaactctc acacttccag	1536
accctgagaa aaaagccacc ctgaatttac ccggcatgca ctcttcagat aagccatgtc	1596
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 <213> Homo sapiens

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 <222> (136)..(1779)

<400> 582

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attgctctaa actgt atg gtg aag ttg gcc aag ggc agg ccc cat ctt agc	171
Met Val Lys Leu Ala Lys Gly Arg Pro His Leu Ser	
1 5 10	

cag tca gta gtt gag acc ttg ttg act caa ttg cac agt gct caa gac	219
Gln Ser Val Val Glu Thr Leu Leu Thr Gln Leu His Ser Ala Gln Asp	
13 18 23 28	

gct gcc cgg att ttg atg tgc cat tgc ctg gca gcc att gcc atg caa	267
Ala Ala Arg Ile Leu Met Cys His Cys Leu Ala Ala Ile Ala Met Gln	
29 34 39 44	

ctg ccg gtg ctg ggt gat ggg atg ctt ggt gac ctc atg gag ctg tac	315
Leu Pro Val Leu Gly Asp Gly Met Leu Gly Asp Leu Met Glu Leu Tyr	
45 50 55 60	

aag gtg att gga cga tca gcc aca gac aag caa caa gaa ctt ctg gtg	363
Lys Val Ile Gly Arg Ser Ala Thr Asp Lys Gln Gln Glu Leu Leu Val	
61 66 71 76	

agt ttg gct act gtg att ttt gtt gca agt cag aag gca ttg tct gtg	411
Ser Leu Ala Thr Val Ile Phe Val Ala Ser Gln Lys Ala Leu Ser Val	

77	82	87	92	
gaa agt aag gca gta att aag cag cag ctt gaa agt gtc tcc aat gga Glu Ser Lys Ala Val Ile Lys Gln Gln Leu Glu Ser Val Ser Asn Gly	459			
93 98 103 108				
tgg act gta tac cgt att gcc aga cag gct tcc aga atg ggt aat cat Trp Thr Val Tyr Arg Ile Ala Arg Gln Ala Ser Arg Met Gly Asn His	507			
109 114 119 124				
gac atg gcc aaa gag ctt tat cag agt ttg ctg act cag gtt gcc tca Asp Met Ala Lys Glu Leu Tyr Gln Ser Leu Leu Thr Gln Val Ala Ser	555			
125 130 135 140				
gaa cat ttc tac ttc tgg cta aat agt ttg aag gag ttt tca cat gca Glu His Phe Tyr Phe Trp Leu Asn Ser Leu Lys Glu Phe Ser His Ala	603			
141 146 151 156				
gaa cag tgt ctc act ggg ttg caa gag gaa aat tat agt tca gca ctt Glu Gln Cys Leu Thr Gly Leu Gln Glu Glu Asn Tyr Ser Ser Ala Leu	651			
157 162 167 172				
tct tgc att gct gaa tct tta aaa ttc tat cac aaa ggg att gct tcc Ser Cys Ile Ala Glu Ser Leu Lys Phe Tyr His Lys Gly Ile Ala Ser	699			
173 178 183 188				
tta aca gca gct agt aca cca ctg aat cct tta agc ttt cag tgt gaa Leu Thr Ala Ala Ser Thr Pro Leu Asn Pro Leu Ser Phe Gln Cys Glu	747			
189 194 199 204				
ttt gta aaa ctc agg att gac ctt tta caa gcc ttc tct caa ctt atc Phe Val Lys Leu Arg Ile Asp Leu Leu Gln Ala Phe Ser Gln Leu Ile	795			
205 210 215 220				
tgt act tgt aat agc ctg aag aca agc cca cca cct gca att gcc aca Cys Thr Cys Asn Ser Leu Lys Thr Ser Pro Pro Pro Ala Ile Ala Thr	843			
221 226 231 236				
aca att gcc atg acc tta gga aat gac ctc cag agg tgt ggt cgc atc Thr Ile Ala Met Thr Leu Gly Asn Asp Leu Gln Arg Cys Gly Arg Ile	891			
237 242 247 252				
tcc aat cag atg aaa cag tcc atg gaa gaa ttt cga agc ctt gct tct Ser Asn Gln Met Lys Gln Ser Met Glu Glu Phe Arg Ser Leu Ala Ser	939			
253 258 263 268				
cga tat gga gat ctt tac cag gca tct ttt gat gct gac tca gca act Arg Tyr Gly Asp Leu Tyr Gln Ala Ser Phe Asp Ala Asp Ser Ala Thr	987			
269 274 279 284				
ttg agg aat gtt gaa cta cag cag cag agc tgt tta ctg ata tct cat Leu Arg Asn Val Glu Leu Gln Gln Ser Cys Leu Leu Ile Ser His	1035			
285 290 295 300				
gca ata gaa gcc ctg att ttg gat cca gaa tca gca agt ttc cag gaa Ala Ile Glu Ala Leu Ile Leu Asp Pro Glu Ser Ala Ser Phe Gln Glu	1083			
301 306 311 316				

tat gga tct act gga aca gcc cat gct gat agt gaa tat gaa aga aga		1131	
Tyr Gly Ser Thr Gly Thr Ala His Ala Asp Ser Glu Tyr Glu Arg Arg			
317	322	327	332
atg atg tct gta tat aat cat gtc ttg gag gag gta gaa tca ctc aat		1179	
Met Met Ser Val Tyr Asn His Val Leu Glu Glu Val Glu Ser Leu Asn			
333	338	343	348
cgg aaa tat acc cct gtt tct tat atg cac aca gca tgc ctc tgc aat		1227	
Arg Lys Tyr Thr Pro Val Ser Tyr Met His Thr Ala Cys Leu Cys Asn			
349	354	359	364
gcc atc att gct ttg ctg aaa gtt ccc ctt tct ttc cag aga tat ttt		1275	
Ala Ile Ile Ala Leu Leu Lys Val Pro Leu Ser Phe Gln Arg Tyr Phe			
365	370	375	380
ttc cag aaa cta cag tct acc agc atc aag ctt gct ctg tca cca tcg		1323	
Phe Gln Lys Leu Gln Ser Thr Ser Ile Lys Leu Ala Leu Ser Pro Ser			
381	386	391	396
ccc cgg aat cct gca gag ccc att gct gtc cag aat aac cag cag ctg		1371	
Pro Arg Asn Pro Ala Glu Pro Ile Ala Val Gln Asn Asn Gln Gln Leu			
397	402	407	412
gcg cta aag gta gag gga gtg gtt cag cac gga tct aaa cca gga ctc		1419	
Ala Leu Lys Val Glu Gly Val Val Gln His Gly Ser Lys Pro Gly Leu			
413	418	423	428
ttc cgc aaa att cag tct gtc tgt ctg aat gtt tct tcc aca ctg cag		1467	
Phe Arg Lys Ile Gln Ser Val Cys Leu Asn Val Ser Ser Thr Leu Gln			
429	434	439	444
agt aaa tct gga caa gac tac aag ata ccc att gac aac atg acc aat		1515	
Ser Lys Ser Gly Gln Asp Tyr Lys Ile Pro Ile Asp Asn Met Thr Asn			
445	450	455	460
gag atg gag caa agg gtt gaa cct cat aat gat tac ttc agt act caa		1563	
Glu Met Glu Gln Arg Val Glu Pro His Asn Asp Tyr Phe Ser Thr Gln			
461	466	471	476
ttt ctg ttg aac ttt gct atc ctt gga aca cac aac att aca gtg gaa		1611	
Phe Leu Leu Asn Phe Ala Ile Leu Gly Thr His Asn Ile Thr Val Glu			
477	482	487	492
tct tct gtg aaa gat gcc aat ggt ata gta tgg aag act ggt ccc aga		1659	
Ser Ser Val Lys Asp Ala Asn Gly Ile Val Trp Lys Thr Gly Pro Arg			
493	498	503	508
act acc ata ttt gta aaa tcc ctg gaa gac cct tat tcc cag caa att		1707	
Thr Thr Ile Phe Val Lys Ser Leu Glu Asp Pro Tyr Ser Gln Gln Ile			
509	514	519	524
cgc tta caa cag cag caa gcc cag cag cca tta cag cag cag cag caa		1755	
Arg Leu Gln Gln Gln Ala Gln Gln Pro Leu Gln Gln Gln Gln Gln			
525	530	535	540

cgc aat gcc tac aca cgg ttt taa ccatggaatg aatgcactgc agactctcaa	1809
Arg Asn Ala Tyr Thr Arg Phe *	
541 546	
gagatcaatc aaattgccag aaacagttt gttttcata tggaataagt attaaagtta	1869
cagtgttagtt catttattca ttgattttt taatgtata ttctggaaaa aattttgttt	1929
tcttaaaaat tttgtctgac agctgggcgt ggttgctcac gcctgtaatc ccagcacttt	1989
gggaggctga ggtggcggc tcacgaggag atcaagacca tcctggctaa cacagtgaaa	2049
ccccgtctcc actaaaaaat acaaaaaaat tagccgagca tgggtggcagg cgccctgttagt	2109
cccagctact tgggaggctg aggcaggaga atggtgtgaa cctgggaggc ggagcttgca	2169
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<400> 583

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atccctcgaa tccaccagca cgagcgtccc accccgcgcct gggacc atg gcc act	175
Met Ala Thr	
1	

gac tca tgg gcc ctg gcg gtg gac gag cag gaa gct gcg gct gag tcg	223
Asp Ser Trp Ala Leu Ala Val Asp Glu Gln Glu Ala Ala Glu Ser	
4 9 14 19	

ttg agc aac ttg cat ctt aag gaa gag aaa atc aaa cca gat acc aat	271
Leu Ser Asn Leu His Leu Lys Glu Glu Lys Ile Lys Pro Asp Thr Asn	
20 25 30 35	

ggt gct gtt gtc aag acc aat gcc aat gca gag aag aca gat gaa gaa	319
Gly Ala Val Val Lys Thr Asn Ala Asn Ala Glu Lys Thr Asp Glu Glu	
36 41 46 51	

gag aaa gag gac aga gct gcc cag tcc tta ctc aac aag ctg atc aga	367
Glu Lys Glu Asp Arg Ala Ala Gln Ser Leu Leu Asn Lys Leu Ile Arg	
52 57 62 67	

agc aac ctt gtt gat aac aca aac caa gtg gaa gtc ctg cag cgg gat	68	73	78	83	415
Ser Asn Leu Val Asp Asn Thr Asn Gln Val Glu Val Leu Gln Arg Asp					
cca aac tcc cct ctg tac tcg gtg aag tct ttt gaa gag ctt cgg ctg	84	89	94	99	463
Pro Asn Ser Pro Leu Tyr Ser Val Lys Ser Phe Glu Glu Leu Arg Leu					
aaa cca cag ctt ctc caa gga gtc tat gcc atg ggt ttc aat cgt cca	100	105	110	115	511
Lys Pro Gln Leu Leu Gln Gly Val Tyr Ala Met Gly Phe Asn Arg Pro					
tcc aag ata caa gag aac gca ttg cca ctg atg ctt gct gag ccc cca	116	121	126	131	559
Ser Lys Ile Gln Glu Asn Ala Leu Pro Leu Met Leu Ala Glu Pro Pro					
cag aac tta att gcc caa tct cag tct ggt act ggt aaa aca gct gcc	132	137	142	147	607
Gln Asn Leu Ile Ala Gln Ser Gln Ser Gly Thr Gly Lys Thr Ala Ala					
ttc gtg ctg gcc atg ctt agc caa gta gaa cct gca aac aaa tac ccc	148	153	158	163	655
Phe Val Leu Ala Met Leu Ser Gln Val Glu Pro Ala Asn Lys Tyr Pro					
cag tgt cta tgt ctc tcc cca acg tat gag ctc gcc ctc caa aca gga	164	169	174	179	703
Gln Cys Leu Cys Leu Ser Pro Thr Tyr Glu Leu Ala Leu Gln Thr Gly					
aaa gtg att gaa caa atg ggc aaa ttt tac cct gaa ctg aag cta gct	180	185	190	195	751
Lys Val Ile Glu Gln Met Gly Lys Phe Tyr Pro Glu Leu Lys Leu Ala					
tat gct gtt cga ggc aat aaa ttg gaa aga ggc cag aag atc agt gag	196	201	206	211	799
Tyr Ala Val Arg Gly Asn Lys Leu Glu Arg Gly Gln Lys Ile Ser Glu					
cag att gtc att ggc acc cct ggg act gtg ctg gac tgg tgc tcc aag	212	217	222	227	847
Gln Ile Val Ile Gly Thr Pro Gly Thr Val Leu Asp Trp Cys Ser Lys					
ctc aag ttc att gat ccc aag aaa atc aag gtg ttt gtt ctg gat gag	228	233	238	243	895
Leu Lys Phe Ile Asp Pro Lys Lys Ile Lys Val Phe Val Leu Asp Glu					
gct gat gtc atg ata gcc act cag ggc cac caa gat cag agc atc cgc	244	249	254	259	943
Ala Asp Val Met Ile Ala Thr Gln Gly His Gln Asp Gln Ser Ile Arg					
atc cag agg atg ctg ccc agg aac tgc cag atg ctg ctt ttc tcc gcc	260	265	270	275	991
Ile Gln Arg Met Leu Pro Arg Asn Cys Gln Met Leu Leu Phe Ser Ala					
acc ttt gaa gac tct gtg tgg aag ttt gcc cag aaa gtg gtc cca gac	276	281	286	291	1039
Thr Phe Glu Asp Ser Val Trp Lys Phe Ala Gln Lys Val Val Pro Asp					
cca aac gtt atc aaa ctg aag cgt gag gaa gag acc ctg gac acc atc					1087

Pro Asn Val Ile Lys Leu Lys Arg Glu Glu Glu Thr Leu Asp Thr Ile			
292	297	302	307
aag cag tac tat gtc ctg tgc agc agc aga gac gag aag ttc cag gcc			1135
Lys Gln Tyr Tyr Val Leu Cys Ser Ser Arg Asp Glu Lys Phe Gln Ala			
308	313	318	323
ttg tgt aac ctc tac ggg gcc atc acc att gct caa gcc atg atc ttc			1183
Leu Cys Asn Leu Tyr Gly Ala Ile Thr Ile Ala Gln Ala Met Ile Phe			
324	329	334	339
tgc cat act cgc aaa aca gct agt tgg ctg gca gca gag ctc tca aaa			1231
Cys His Thr Arg Lys Thr Ala Ser Trp Leu Ala Ala Glu Leu Ser Lys			
340	345	350	355
gaa ggc cac cag gtg gct ctg ctg agt ggg gag atg atg gtg gaa cag			1279
Glu Gly His Gln Val Ala Leu Leu Ser Gly Glu Met Met Val Glu Gln			
356	361	366	371
agg gct gca gtg att gag cgc ttc cga gag ggc aaa gag aag gtt ttg			1327
Arg Ala Ala Val Ile Glu Arg Phe Arg Glu Gly Lys Glu Lys Val Leu			
372	377	382	387
gtg acc acc aac gtg tgt gcc cgc ggc att gat gtt gaa caa gtg tct			1375
Val Thr Thr Asn Val Cys Ala Arg Gly Ile Asp Val Glu Gln Val Ser			
388	393	398	403
gtc gtc atc aac ttt gat ctt ccc gtg gac aag gac ggg aat cct gac			1423
Val Val Ile Asn Phe Asp Leu Pro Val Asp Lys Asp Gly Asn Pro Asp			
404	409	414	419
aat gag acc tac ctg cac cgg atc ggg cgc acg ggc cgc ttt ggc aag			1471
Asn Glu Thr Tyr Leu His Arg Ile Gly Arg Thr Gly Arg Phe Gly Lys			
420	425	430	435
agg ggc ctg gca gtg aac atg gtg gac agc aag cac agc atg aac atc			1519
Arg Gly Leu Ala Val Asn Met Val Asp Ser Lys His Ser Met Asn Ile			
436	441	446	451
ctg aac aga atc cag gag cat ttt aat aag aag ata gaa aga ttg gac			1567
Leu Asn Arg Ile Gln Glu His Phe Asn Lys Lys Ile Glu Arg Leu Asp			
452	457	462	467
aca gat gat ttg gac gag att gag aaa ata gcc aac tga gaagctccac			1616
Thr Asp Asp Leu Asp Glu Ile Glu Lys Ile Ala Asn *			
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 tgctatcatt tccgcaggcc agatcagaaa agggagctca ggtacacctcc agagagttag 180
 acccagcgcc cttgtctcgc acccagtagg ctttcatccc cgcc atg gct gag ctg 236
 Met Ala Glu Leu
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atc cag aag aag cta cag gga gaa gtg gag aaa tat caa cag cta cag 284
 Ile Gln Lys Lys Leu Gln Gly Glu Val Glu Lys Tyr Gln Gln Leu Gln
 5 10 15 20

aag gac tta agt aaa tcc atg tcg ggg agg cag aaa ctt gaa gca caa 332
 Lys Asp Leu Ser Lys Ser Met Ser Gly Arg Gln Lys Leu Glu Ala Gln
 21 26 31 36

cta aca gaa aat aat atc gtg aaa gag gaa ctg gcc ctg ctg gat ggg 380
 Leu Thr Glu Asn Asn Ile Val Lys Glu Glu Leu Ala Leu Leu Asp Gly
 37 42 47 52

tcc aac gtg gtc ttt aaa ctt ctg ggt ccg gtg cta gtc aaa cag gag 428
 Ser Asn Val Val Phe Lys Leu Leu Gly Pro Val Leu Val Lys Gln Glu
 53 58 63 68

ctg ggg gag gct cgg gcc aca gta ggg aag agg ctg gac tat atc aca 476
 Leu Gly Glu Ala Arg Ala Thr Val Gly Lys Arg Leu Asp Tyr Ile Thr
 69 74 79 84

gct gaa att aag cga tac gaa tcc cag ctt cgg gat ctt gag cgg cag 524
 Ala Glu Ile Lys Arg Tyr Glu Ser Gln Leu Arg Asp Leu Glu Arg Gln
 85 90 95 100

tca gag caa cag agg gag acc ctt gct cag ctg cag cag gag ttc cag 572
 Ser Glu Gln Gln Arg Glu Thr Leu Ala Gln Leu Gln Glu Phe Gln
 101 106 111 116

cgg gcc cag gca gca aag gca ggg gct cct ggc aag gcc tga cccatg	621
Arg Ala Gln Ala Ala Lys Ala Gly Ala Pro Gly Lys Ala *	
117 122 127	
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Met Ala Glu Leu	
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Ile Gln Lys Lys Leu Gln Gly Glu Val Glu Lys Tyr Gln Gln Leu Gln	
5 10 15 20	
aag gac tta agt aaa tcc atg tcg ggg agg cag aaa ctt gaa gca caa	332
Lys Asp Leu Ser Lys Ser Met Ser Gly Arg Gln Lys Leu Glu Ala Gln	
21 26 31 36	
cta aca gaa aat aat atc gtg aaa gag gtg agg gac tgg gat ttg tgg	380
Leu Thr Glu Asn Asn Ile Val Lys Glu Val Arg Asp Trp Asp Leu Trp	
37 42 47 52	
ggc gag gga cct gta cta gcc atg gtt ctg atc aca tat gtc cca	428
Gly Glu Glu Gly Pro Val Leu Ala Met Val Leu Ile Thr Tyr Val Pro	
53 58 63 68	
tcc ctc cat cag gaa ctg gcc ctg ctg gat ggg tcc aac gtg gtc ttt	476
Ser Leu His Gln Glu Leu Ala Leu Leu Asp Gly Ser Asn Val Val Phe	
69 74 79 84	
aaa ctt ctg ggt ccg gtg cta gtc aaa cag gag ctg ggg gag gct cgg	524
Lys Leu Leu Gly Pro Val Leu Val Lys Gln Glu Leu Gly Glu Ala Arg	

85	90	95	100	
gcc aca gta ggg aag agg ctg gac tat atc aca gct gaa att aag cga Ala Thr Val Gly Lys Arg Leu Asp Tyr Ile Thr Ala Glu Ile Lys Arg 101 106 111 116				572
tac gaa tcc cag ctt cg ^g gat ctt gag cg ^g cag tca gag caa cag agg Tyr Glu Ser Gln Leu Arg Asp Leu Glu Arg Gln Ser Glu Gln Gln Arg 117 122 127 132				620
gag acc ctt gct cag ctg cag cag gag ttc cag cg ^g gcc cag gca gca Glu Thr Leu Ala Gln Leu Gln Gln Glu Phe Gln Arg Ala Gln Ala Ala 133 138 143 148				668
aag gca ggg gct cct ggc aag gcc tga cccca tggtgggggg aggggagggg Lys Ala Gly Ala Pro Gly Lys Ala *149 154				720
aggggagggga atgaggcagc tctaggatct atactgtac taataaaatg taaaaaacacc tgaaaaaaaaaaa aaaagtgcac cggccgcgaa tttagtagta gtggcgccg cgtctagagg atccaagctt acgtacgcgt gcatgcgacg tcatactct tctatagtgt cacctaaatt caattca				780 840 900 907
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Leu Leu Asp Ile Arg His Glu Lys Ile Pro Ile Gly Glu Lys Ser Tyr	
31 36 41 46	
aaa tat gat caa aaa agg aat gcc att aat tat cac cag gat ctc agt	494
Lys Tyr Asp Gln Lys Arg Asn Ala Ile Asn Tyr His Gln Asp Leu Ser	
47 52 57 62	
cag cca agt ttt ggc caa tct ttt gag tat agt aaa aat gga caa ggc	542
Gln Pro Ser Phe Gly Gln Ser Phe Glu Tyr Ser Lys Asn Gly Gln Gly	
63 68 73 78	
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Phe His Asp Glu Ala Ala Phe Phe Thr Asn Lys Arg Ser Gln Ile Gly	
79 84 89 94	
gag aca gtc tgt aaa tat aac gaa tgt gga aga acc ttc att gaa agt	638
Glu Thr Val Cys Lys Tyr Asn Glu Cys Gly Arg Thr Phe Ile Glu Ser	
95 100 105 110	
tta aag ctg aat ata tct caa aga cct cat ttg gaa atg gag ccg tat	686
Leu Lys Leu Asn Ile Ser Gln Arg Pro His Leu Glu Met Glu Pro Tyr	
111 116 121 126	
gga tgc agt att tgc ggg aag tcc ttc tgc atg aat tta agg ttt gga	734
Gly Cys Ser Ile Cys Gly Lys Ser Phe Cys Met Asn Leu Arg Phe Gly	
127 132 137 142	
cat cag aga gct ctt aca aag gac aat cct tat gaa tat aat gaa tat	782
His Gln Arg Ala Leu Thr Lys Asp Asn Pro Tyr Glu Tyr Asn Glu Tyr	
143 148 153 158	
ggg gaa atc ttc tgt gac aat tca gct ttc att atc cat cag gga gct	830
Gly Glu Ile Phe Cys Asp Asn Ser Ala Phe Ile Ile His Gln Gly Ala	
159 164 169 174	
tac aca aga aag att ctc cgt gaa tat aaa gtg agt gac aaa acc tgg	878
Tyr Thr Arg Lys Ile Leu Arg Glu Tyr Lys Val Ser Asp Lys Thr Trp	
175 180 185 190	
gaa aag tca gct ctc tta aaa cat caa ata gta cac atg ggg gga aag	926
Glu Lys Ser Ala Leu Leu Lys His Gln Ile Val His Met Gly Gly Lys	
191 196 201 206	
tct tat gat tac aat gaa aat ggg agt aat ttc agc aag aag tca cat	974
Ser Tyr Asp Tyr Asn Glu Asn Gly Ser Asn Phe Ser Lys Lys Ser His	
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Leu Thr Gln Leu Arg Arg Ala His Thr Gly Glu Lys Thr Phe Glu Cys	
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239 244 249 254	/
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Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Thr Glu Cys Gly			
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Lys Ala Phe Cys Gln Lys Pro His Leu Thr Asn His Gln Arg Thr His			
271	276	281	286
aca gga gaa aaa ccc tat gaa tgt aag caa tgt gga aaa aca ttc tgc			1214
Thr Gly Glu Lys Pro Tyr Glu Cys Lys Gln Cys Gly Lys Thr Phe Cys			
287	292	297	302
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Val Lys Ser Asn Leu Thr Glu His Gln Arg Thr His Thr Gly Glu Lys			
303	308	313	318
ccc tat gaa tgt aat gca tgt ggg aaa tcc ttc tgc cac aga tca gcc			1310
Pro Tyr Glu Cys Asn Ala Cys Gly Lys Ser Phe Cys His Arg Ser Ala			
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ctc act gtg cat cag aga aca cac aca ggg gag aaa ccg ttt ata tgt			1358
Leu Thr Val His Gln Arg Thr His Thr Gly Glu Lys Pro Phe Ile Cys			
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Asn Glu Cys Gly Lys Ser Phe Cys Val Lys Ser Asn Leu Ile Val His			
351	356	361	366
caa aga act cac act ggg gag aaa cca tat aag tgt aat gaa tgt ggg			1454
Gln Arg Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly			
367	372	377	382
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Lys Thr Phe Cys Glu Lys Ser Ala Leu Thr Lys His Gln Arg Thr His			
383	388	393	398
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Thr Gly Glu Lys Pro Tyr Glu Cys Asn Ala Cys Gly Lys Thr Phe Ser			
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cag agg tca gtg ctc acc aaa cat cag aga att cac aca agg gtg aaa			1598
Gln Arg Ser Val Leu Thr Lys His Gln Arg Ile His Thr Arg Val Lys			
415	420	425	430
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Gly Val Gly Lys Ser Ser Ile Val Trp Arg Phe Val Glu Asp Ser Phe	
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Asp Pro Asn Ile Asn Pro Thr Ile Gly Ala Ser Phe Met Thr Lys Thr	
31 36 41 46	

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gaa gtc atg gag aga gat gca aag gac tac gcc gac tct att cat gca Glu Val Met Glu Arg Asp Ala Lys Asp Tyr Ala Asp Ser Ile His Ala 127 132 137 142	491
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caaggaagta tgccgagatt ttgctgtcct ggaggaccac accctggctc acagcctgca	180
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atg gcc cac agg gat cag	
Met Ala His Arg Asp Gln	
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Glu Trp Tyr Asp Ala Glu Ile Ala Arg Lys Leu Gln Glu Glu Leu	
7 12 17 22	
ttg gct acc cag gtg gac atg aga gcc gct caa gta gct caa gat gaa	688
Leu Ala Thr Gln Val Asp Met Arg Ala Ala Gln Val Ala Gln Asp Glu	
23 28 33 38	
gaa atc gct cga / ctt cta atg gct gaa gaa aag aaa gct tac aaa aaa	736
Glu Ile Ala Arg Leu Leu Met Ala Glu Glu Lys Lys Ala Tyr Lys Lys	
39 44 49 54	

gcc aag gag cg ^g gag aaa tca tct ttg gac aaa aga aag caa gac ccc Ala Lys Glu Arg Glu Lys Ser Ser Leu Asp Lys Arg Lys Gln Asp Pro 55 60 65 70	784
gag tgg aag cca aaa aca gct aaa gca gca aat tca aag tca aaa gag Glu Trp Lys Pro Lys Thr Ala Lys Ala Asn Ser Lys Ser Lys Glu 71 76 81 86	832
agt gat gaa cct cac cat tct aag aat gaa agg cca gca cg ^g cca cca Ser Asp Glu Pro His His Ser Lys Asn Glu Arg Pro Ala Arg Pro Pro 87 92 97 102	880
cca cct atc atg aca gat ggt gaa gat gcg gat tac act cat ttt aca Pro Pro Ile Met Thr Asp Gly Glu Asp Ala Asp Tyr Thr His Phe Thr 103 108 113 118	928
aac cag cag agt tcc aca cg ^g cat ttc tca aaa tca gag tcc tct cat Asn Gln Gln Ser Ser Thr Arg His Phe Ser Lys Ser Glu Ser Ser His 119 124 129 134	976
aaa ggt ttt cat tac aaa cat taa aaaccttagga atctgccttg aaaatggact Lys Gly Phe His Tyr Lys His *	1030
cactatagca aatattactg ggtgatacag aatgaattct acacttactt tttttctcct	1090
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Met Ser Gly Leu			
1			
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Val Leu Gly Gln Arg Asp Glu Pro Ala Gly His Arg Leu Ser Gln Glu			
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gag atc ctg ggg agc aca cgg ctg gtc agc caa ggg cta gag gcc cta	209		
Glu Ile Leu Gly Ser Thr Arg Leu Val Ser Gln Gly Leu Glu Ala Leu			
21	26	31	36
cgc agt gaa cac cag gcc gtg ctg caa agc ctg tcc cag acc att gag	257		
Arg Ser Glu His Gln Ala Val Leu Gln Ser Leu Ser Gln Thr Ile Glu			
37	42	47	52
tgt ctg cag cag gga ggc cat gag gaa ggg ctg gtg cat gag aag gcc	305		
Cys Leu Gln Gln Gly His Glu Glu Gly Leu Val His Glu Lys Ala			
53	58	63	68
cgc cag ctt cgc cgt tct atg gaa aac att gag ctc ggg ctg agt gag	353		
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69	74	79	84
gcc cag gtg atg ctg gct cta gcc agc cac ctg agc aca gtg gag tcg	401		
Ala Gln Val Met Leu Ala Leu Ala Ser His Leu Ser Thr Val Glu Ser			
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gag aaa cag aag ctg cgg gct cag gtg cgg cgg cta tgc cag gag aac	449		
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Gln Trp Leu Arg Asp Glu Leu Ala Gly Thr Gln Gln Arg Leu Gln Arg			
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agt gaa cag gct gtg gct cag ctg gag gag gaa aag aag cac ctg gag	545		
Ser Glu Gln Ala Val Ala Gln Leu Glu Glu Lys Lys His Leu Glu			
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ttc ctg ggg cag ctg cgg cag tat gat gag gat gga cat acc tcg gag	593		
Phe Leu Gly Gln Leu Arg Gln Tyr Asp Glu Asp Gly His Thr Ser Glu			
149	154	159	164
gag aaa gaa ggc gat gcc acc aag gat tcc ctg gat gac ctc ttt cct	641		
Glu Lys Glu Gly Asp Ala Thr Lys Asp Ser Leu Asp Asp Leu Phe Pro			
165	170	175	180
aat gag gag gaa gag gac ccc agc aat ggc ttg tcc cgt ggt caa ggt	689		
Asn Glu Glu Glu Asp Pro Ser Asn Gly Leu Ser Arg Gly Gln Gly			
181	186	191	196
gct aca gca gct cag cag ggt gga tat gag atc cca gca agg ttg cgg	737		
Ala Thr Ala Ala Gln Gln Gly Gly Tyr Glu Ile Pro Ala Arg Leu Arg			
197	202	207	212
acg ttg cac aac ctg gtg atc cag tac gca gcc caa ggt cgc tat gag	785		
Thr Leu His Asn Leu Val Ile Gln Tyr Ala Ala Gln Gly Arg Tyr Glu			

213	218	223	228	
gtg gcc gtg cca ctc tgt aag cag gca cta gag gac ctg gag cgc aca Val Ala Val Pro Leu Cys Lys Gln Ala Leu Glu Asp Leu Glu Arg Thr				833
229 234 239 244				
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245 250 255 260				
ttg gtg tat cgt gac cag aat aag tat aag gaa gct gcc cac ctg ctg Leu Val Tyr Arg Asp Gln Asn Lys Tyr Lys Glu Ala Ala His Leu Leu				929
261 266 271 276				
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277 282 287 292				
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293 298 303 308				
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373 378 383 388				
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389 394 399 404				
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405 410 415 420				
cac aag ccc atc tgg atg cat gca gag gag cgg gag gaa atg agc aaa His Lys Pro Ile Trp Met His Ala Glu Glu Arg Glu Glu Met Ser Lys				1409
421 426 431 436				
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437 442 447 452				

tac aag gcc tgc aaa gtg agc agc ccc aca gtg aac act act ctg aga	453	458	463	468	1505
Tyr Lys Ala Cys Lys Val Ser Ser Pro Thr Val Asn Thr Thr Leu Arg					
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Asn Leu Gly Ala Leu Tyr Arg Arg Gln Gly Lys Leu Glu Ala Ala Glu					
acc ctg gag gaa tgt gcc ctg cgg tcc cgg aga cag ggc act gac cct	485	490	495	500	1601
Thr Leu Glu Glu Cys Ala Leu Arg Ser Arg Arg Gln Gly Thr Asp Pro					
atc agc cag acg aaa gca gct gac att caa ccc ggc ccc cag gtc tgc	501	506	511	516	1649
Ile Ser Gln Thr Lys Ala Ala Asp Ile Gln Pro Gly Pro Gln Val Cys					
tgg tcc ccc gtc ccc cac agc cct cac agc att ccc cat tgc tcc tgg	517	522	527	532	1697
Trp Ser Pro Val Pro His Ser Pro His Ser Ile Pro His Cys Ser Trp					
ctc ttc ctc tcc cct agg tgg gac agt gaa ggg gag cag ttt aac cag	533	538	543	548	1745
Leu Phe Leu Ser Pro Arg Trp Asp Ser Glu Gly Glu Gln Phe Asn Gln					
aag att gct gct gcc ctt agg gtc tca gct ccc tcc tct gga atc cct	549	554	559	564	1793
Lys Ile Ala Ala Ala Leu Arg Val Ser Ala Pro Ser Ser Gly Ile Pro					
ctt agg aag gac cct cag gac acc ctc tct gca ccc tgt ggt cct cta	565	570	575	580	1841
Leu Arg Lys Asp Pro Gln Asp Thr Leu Ser Ala Pro Cys Gly Pro Leu					
gag tag ctagctctga ggccccagg tgggtacaaa gcaggtatgg ccctcagaga	581				1897
Glu *					
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8 13 18 23	
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24 29 34 39	
ttc tca aat gtg cct gaa aga gac ctt tca aat gta tct aac ata cat Phe Ser Asn Val Pro Glu Arg Asp Leu Ser Asn Val Ser Asn Ile His	318
40 45 50 55	
tcc agt ttt gca act tct cca act gga gct tca aac agc aag tat gtt Ser Ser Phe Ala Thr Ser Pro Thr Gly Ala Ser Asn Ser Lys Tyr Val	366
56 61 66 71	
tca gct gat aga aat ctc atc aag aat act gcc cca gtg aac act gta Ser Ala Asp Arg Asn Leu Ile Lys Asn Thr Ala Pro Val Asn Thr Val	414
72 77 82 87	
atg gac agt cca gtg cat tta gag cca tct agt cag gtt ggt gtg atc Met Asp Ser Pro Val His Leu Glu Pro Ser Ser Gln Val Gly Val Ile	462
88 93 98 103	
cag aat aaa tca tgg gag atg cct gtt gat aga cta gag aca tta agc Gln Asn Lys Ser Trp Glu Met Pro Val Asp Arg Leu Glu Thr Leu Ser	510
104 109 114 119	
acc aga gac ttt atc tgc cca aat tct aac ata cct gat caa gaa tcc Thr Arg Asp Phe Ile Cys Pro Asn Ser Asn Ile Pro Asp Gln Glu Ser	558
120 125 130 135	
tct ctt cag agt ttt tgt aat tct gaa aat aag gta ttg aaa gaa aat Ser Leu Gln Ser Phe Cys Asn Ser Glu Asn Lys Val Leu Lys Glu Asn	606
136 141 146 151	
gct gat ttt tta tcc ctg cgc cag act gaa ctg cca gga aac tct tgt Ala Asp Phe Leu Ser Leu Arg Gln Thr Glu Leu Pro Gly Asn Ser Cys	654
152 157 162 167	
gct cag gat ccg gca tcc ttt atg cct cca cag cag cct tgc tct ttc Ala Gln Asp Pro Ala Ser Phe Met Pro Pro Gln Gln Pro Cys Ser Phe	702
168 173 178 183	
ccc agc caa tca ctt tca gat gct gaa tcg att tct aaa cat atg tct Pro Ser Gln Ser Leu Ser Asp Ala Glu Ser Ile Ser Lys His Met Ser	750
184 189 194 199	
ttg tca tat gtt gct aat caa gag cca ggt att tta caa caa aaa aat Leu Ser Tyr Val Ala Asn Gln Glu Pro Gly Ile Leu Gln Gln Lys Asn	798

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gcc ttt gtc cca gtg tac tct gac agc act att caa gaa gca tca cca Ala Phe Val Pro Val Tyr Ser Asp Ser Thr Ile Gln Glu Ala Ser Pro 248 253 258 263				942
aac ttt gag aaa gct tat act tta cct gtg tta cca tca gaa aag gac Asn Phe Glu Lys Ala Tyr Thr Leu Pro Val Leu Pro Ser Glu Lys Asp 264 269 274 279				990
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aca act gat act cag gtc att tca cat gaa aaa gaa aac aaa ctg gag Thr Thr Asp Thr Gln Val Ile Ser His Glu Lys Glu Asn Lys Leu Glu 312 317 322 327				1134
agt ttg gtt tta act cat ttg agt agg tgt gat tct gat tta tgt gaa Ser Leu Val Leu Thr His Leu Ser Arg Cys Asp Ser Asp Leu Cys Glu 328 333 338 343				1182
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cat tgt cct gaa agt gaa aag tgt ttg ctt tcc ata gaa gat gag gaa His Cys Pro Glu Ser Glu Lys Cys Leu Leu Ser Ile Glu Asp Glu Glu 360 365 370 375				1278
tct caa caa agc att tta tca agt ctg gaa aac cat tca cag cag tca Ser Gln Gln Ser Ile Leu Ser Ser Leu Glu Asn His Ser Gln Gln Ser 376 381 386 391				1326
act caa cca gaa atg cat aaa tat ggt cag tta gtt aaa gta gaa tta Thr Gln Pro Glu Met His Lys Tyr Gly Gln Leu Val Lys Val Glu Leu 392 397 402 407				1374
gaa gaa aat gcc gaa gat gat aaa act gaa aac caa atc cct caa aga Glu Glu Asn Ala Glu Asp Asp Lys Thr Glu Asn Gln Ile Pro Gln Arg 408 413 418 423				1422
atg act aga aac aaa gca aat aca atg gca aat caa agc aaa cag att Met Thr Arg Asn Lys Ala Asn Thr Met Ala Asn Gln Ser Lys Gln Ile 424 429 434 439				1470

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cct aga gga aga ata aga tta act gaa gat gac gat cct caa att cac Pro Arg Gly Arg Ile Arg Leu Thr Glu Asp Asp Asp Pro Gln Ile His 456 461 466 471	1566
cat cca cgg aaa agg aaa gtg tca cgt gta cct cag cct gtg caa gtg His Pro Arg Lys Arg Lys Val Ser Arg Val Pro Gln Pro Val Gln Val 472 477 482 487	1614
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gcc att gta gat tct cta aaa cta gat gag att cag cca tac agt tca Ala Ile Val Asp Ser Leu Lys Leu Asp Glu Ile Gln Pro Tyr Ser Ser 504 509 514 519	1710
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Thr Ser Val Arg Asp Arg Phe Asn Ala Arg Gln Phe Met Ser Trp Leu	
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Gln Asp Val Asp Asp Lys Phe Asp Lys Leu Lys Thr Cys Leu Leu Met	
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Arg Gln Gln His Glu Ala Ala Ala Leu Asn Ala Val Gln Arg Leu Glu	
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Trp Gln Leu Lys Leu Gln Glu Leu Asp Pro Ala Thr Tyr Lys Ser Ile	
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Ser Ile Tyr Glu Ile Gln Glu Phe Tyr Val Pro Leu Val Asp Val Asn	
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Pro Glu Ile His Met Thr Gly Pro Met Cys Leu Ile Glu Asn Thr Asn					
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Gly Glu Leu Val Ala Asn Pro Glu Ala Leu Lys Ile Leu Ser Ala Ile					
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Thr Gln Pro Val Val Val Ala Ile Val Gly Leu Tyr Arg Thr Gly					
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Lys Ser Tyr Leu Met Asn Lys Leu Ala Gly Lys Lys Lys Gly Phe Ser					
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Leu Gly Ser Thr Val Gln Ser His Thr Lys Gly Ile Trp Met Trp Cys					
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Val Pro His Pro Lys Lys Pro Gly His Ile Leu Val Leu Leu Asp Thr					
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